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GenCore version 5.1.6

(without alignments)

Run on: April 15, 2005, 14:09:02 ; Search time 137 Seconds

713.263 Million cell updates/sec

Title: US-10-809-655-9
Perfect score: 1528
Sequence: 1 MSPRGTCGCSAGLMLTVGWLIL.....LDQQLPTEMPGDDALESEWN 294

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 33237063 residues
Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:
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9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:
10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:
11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:
12: /cgn2_6/ptodata/2/pubpaa/US10_PUB.pep:
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1528	100.0	294	14 US-10-181-642-9 Sequence 9, AppI
2	1528	100.0	294	16 US-10-809-655-9 Sequence 9, AppI
3	1528	100.0	294	16 US-10-809-655-9 Sequence 9, AppI
4	762.5	49.9	163	14 US-10-411-224-105 Sequence 105, App
5	762.5	49.9	163	15 US-10-047-021-105 Sequence 119, App
6	593	38.8	124	15 US-10-047-021-105 Sequence 119, App
7	593	38.8	125	14 US-10-411-224-119 Sequence 119, App
8	7.2	1315	15	15 US-10-369-493-3346 Sequence 3346, App
9	7.2	103	25	11 US-10-833-245-1568 Sequence 1568, App
10	100	6.5	604	16 US-10-437-963-174055 Sequence 174055, App
11	99	6.5	255	11 US-09-833-245-1567 Sequence 1567, App
12	99	6.5	255	13 US-10-052-586-538 Sequence 538, App
13	6.5	255	14 US-10-174-590-538 Sequence 538, App	

14 99 6.5 255 14 US-10-176-758-538
15 99 6.5 255 14 US-10-175-737-538
16 99 6.5 255 14 US-10-174-581-538
17 99 6.5 255 14 US-10-176-483-538
18 99 6.5 255 14 US-10-176-749-538
19 99 6.5 255 14 US-10-176-914-538
20 99 6.5 255 14 US-10-176-915-538
21 99 6.5 255 14 US-10-173-706-538
22 99 6.5 255 14 US-10-175-738-538
23 99 6.5 255 14 US-10-175-752-538
24 99 6.5 255 14 US-10-176-482-538
25 99 6.5 255 14 US-10-176-757-538
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27 99 6.5 255 14 US-10-180-552-538
28 99 6.5 255 14 US-10-180-557-538
29 99 6.5 255 14 US-10-173-700-538
30 99 6.5 255 14 US-10-174-572-538
31 99 6.5 255 14 US-10-174-573-538
32 99 6.5 255 14 US-10-174-582-538
33 99 6.5 255 14 US-10-174-588-538
34 99 6.5 255 14 US-10-175-739-538
35 99 6.5 255 14 US-10-175-740-538
36 99 6.5 255 14 US-10-175-741-538
37 99 6.5 255 14 US-10-176-480-538
38 99 6.5 255 14 US-10-176-492-538
39 99 6.5 255 14 US-10-176-500-538
40 99 6.5 255 14 US-10-176-750-538
41 99 6.5 255 14 US-10-176-985-538
42 99 6.5 255 14 US-10-176-987-538
43 99 6.5 255 14 US-10-176-992-538
44 99 6.5 255 14 US-10-176-993-538
45 99 6.5 255 14 US-10-184-658-538

RESULT 1
US-10-181-642-9
; Sequence 9, Application US/10181642
; Publication No. US20030087375A1

; GENERAL INFORMATION:

; APPLICANT: Herr, John C.
; APPLICANT: Shetty, Jagathapala.
; APPLICANT: Wołkowicz, Michael.
; APPLICANT: Jayes, Friederike.
; APPLICANT: Hao, Zhonglin.
; TITLE OF INVENTION: Sperm specific Proteins

; FILE REFERENCE: 00497-02
; CURRENT APPLICATION NUMBER: US/10/181,642

; PRIORITY FILING DATE: 2002-07-19
; RECORDEDING DATE: 2003-01-19
; NUMBER OF SEQIDS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 294

; TYPE: PRT

; ORGANISM: Homo sapiens
; US-10-181-642-9

Query Match Similarity 100.0%; Score 1528; DB 14; Length 294;

Best Local Similarity 100.0%; Pred. No. 5e-150; Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSPRGTCGCSAGLMLTVGWLIL.....LDQQLPTEMPGDDALESEWN 294

Db 1 MSPRGTCGCSAGLMLTVGWLIL.....LDQQLPTEMPGDDALESEWN 294

QY 61 NYARPPETEDSVNENWVKEVEFNGCTVIGIGREVILINGCPGGSKCVWRVERCRGPID 120

Db 61 NYARPPETEDSVNENWVKEVEFNGCTVIGIGREVILINGCPGGSKCVWRVERCRGPID 120

Qy 121 CGWCKPISLESVRLACHTSPNPKMMKLQRDQOSITLVDNSATLEVREKESHLA 180
 Db 121 CGWCKPISLESVRLACHTSPNPKMMKLQRDQOSITLVDNSAILEVRKESHLA 180
 Qy 181 FEGCDLNNEIVATIKFTVTTSSLQMRSSSLPATDAALIFVLTIGVIVCVRIFLIFI 240
 Db 181 FEGCDLNNEIVATIKFTVTTSSLQMRSSSLPATDAALIFVLTIGVIVCVRIFLIFI 240
 Qy 241 IINWAAVKAFWGAKASTPEVQSBRSVRYKDSLSQDQPTMPGDDALEMENE 294
 Db 241 IINWAAVKAFWGAKASTPEVQSBRSVRYKDSLSQDQPTMPGDDALEMENE 294

FILE REFERENCE: 00497-02
 CURRENT APPLICATION NUMBER: US/104809655
 CURRENT FILING DATE: 2004-03-25
 PRIOR APPLICATION NUMBER: 60/176,885
 PRIOR FILING DATE: 2000-01-19
 NUMBER OF SEQ ID NOS: 20
 SRQ ID NO: 9
 LENGTH: 294
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-809-655-9

RESULT 2
 US-10-809-654-9
 ; Sequence 9, Application US/10809654
 ; Publication No. US20040161824A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herr, John C.
 ; APPLICANT: Shetty, Jagathapala
 ; APPLICANT: Wolkowicz, Michael
 ; APPLICANT: Jaynes, Friederike
 ; APPLICANT: Hao, Zhonglin
 ; TITLE OF INVENTION: Sperm Specific Proteins
 ; FILE REFERENCE: 00497-02
 ; CURRENT APPLICATION NUMBER: US/10/809,654
 ; CURRENT FILING DATE: 2004-03-25
 ; PRIOR APPLICATION NUMBER: 60/176,885
 ; PRIOR FILING DATE: 2000-01-19
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO: 9
 ; LENGTH: 294
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-809-654-9

Query Match 100.0%; Score 1528; DB 16; Length 294;
 Best Local Similarity 100.0%; Pred. No. 5e-150; Mismatches 0; Indels 0; Gaps 0;

Matches 294; Conservative 0; MisMatches 0; Indels 0; Gaps 0;
 1 MSPRGTGCSAGLMTVGMLLAGIQLQSARGNTTAAYODAGLAHHRGGRERETENDSETAE 60
 Db 1 MSPRGTGCSAGLMTVGMLLAGIQLQSARGNTTAAYODAGLAHHRGGRERETENDSETAE 60
 Qy 61 NYAPRPETEVSNRNVYKEVFGMCVTCGIGVRVILNGCPGERSKCVVRERCGPFD 120
 Db 61 NYAPRPETEVSNRNVYKEVFGMCVTCGIGVRVILNGCPGERSKCVVRERCGPFD 120
 Qy 121 CGWCKPISLESVRLACHTSPNPKMMKLQRDQOSITLVDNSAILEVRKESHLA 180
 Db 121 CGWCKPISLESVRLACHTSPNPKMMKLQRDQOSITLVDNSAILEVRKESHLA 180
 Qy 181 FEGCDLNNEIVATIKFTVTTSSLQMRSSSLPATDAALIFVLTIGVIVCVRIFLIFI 240
 Db 181 FEGCDLNNEIVATIKFTVTTSSLQMRSSSLPATDAALIFVLTIGVIVCVRIFLIFI 240
 Qy 241 IINWAAVKAFWGAKASTPEVQSBRSVRYKDSLSQDQPTMPGDDALEMENE 294
 Db 241 IINWAAVKAFWGAKASTPEVQSBRSVRYKDSLSQDQPTMPGDDALEMENE 294

RESULT 4
 US-10-411-224-105

; Sequence 105, Application US/10411224
 ; Publication No. US20030166906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 50 Human Secreted Proteins
 ; FILE REFERENCE: P2016_P1
 ; CURRENT APPLICATION NUMBER: US/10/411,224
 ; CURRENT FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: US/09/722,329
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/262,109
 ; PRIOR FILING DATE: 1999-03-04
 ; PRIOR APPLICATION NUMBER: 60/057,626
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/057,663
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/057,669
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/058,667
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,974
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,973
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,666
 ; PRIOR FILING DATE: 1997-09-12

PRIOR APPLICATION NUMBER: 60/090,112
 PRIOR FILING DATE: 1998-06-22
 NUMBER OF SEQ ID NOS: 206
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO: 105
 LENGTH: 163
 TYPE: PRT

RESULT 3

US-10-809-655-9

; Sequence 9, Application US/10809655
 ; Publication No. US20040161825A1

; GENERAL INFORMATION:
 ; APPLICANT: Herr, John C.
 ; APPLICANT: Shetty, Jagathapala
 ; APPLICANT: Wolkowicz, Michael
 ; APPLICANT: Jaynes, Friederike
 ; APPLICANT: Hao, Zhonglin
 ; TITLE OF INVENTION: Sperm Specific Proteins

ORGANISM: Homo sapiens
 FEATURE: SITE
 NAME/KEY: SITE
 LOCATION: (106)
 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-10-411-224-105

Query Match 49.9%; Score 762.5; DB 14; Length 163;
 Best Local Similarity 94.2%; Pred. No. 9e-71; Mismatches 6; Indels 1; Gaps 1;
 Matches 147; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

QY 1 MSPRGTGCGSAGLMLTVGMILLAGIQSARGNTVTAQDAGLAHGEGERETENDSETAE 60
 Db 1 MSPRGTGCGSAGLMLTVGMILLAGIQSARGNTVTAQDAGLAHGEGERETENDSETAE 60

QY 61 NYAPPETEDVSNRNVKVEFGMCTVTGIGVREVILTINGCPGGESKCVVRVERCRGPTD 120
 Db 61 NYAPPETEDVSNRNVKVEFGMCTVTGIGVREVILTINGCPGGESKCVVRVERCRGPTD 120

QY 61 NYAPPETEDVSNRNVKVEFGMCTVTGIGVREVILTINGCPGGESKCVVRVERCRGPTD 120
 Db 61 NYAPPETEDVSNRNVKVEFGMCTVTGIGVREVILTINGCPGGESKCVVRVERCRGPTD 120

121 CGMKPKPISLESVRLACHTSPNPKMKWLRQ 155
 121 CGMKPKPISLESVRLACHTSPNPKMKWLRQ 155

RESULT 5
 US-10-047-021-105
 Sequence 105, Application US/10047021
 Publication No. US20040002591A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 50 Human Secreted Proteins
 FILE REFERENCE: PZ016P2
 CURRENT APPLICATION NUMBER: US/10/047,021
 CURRENT FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: US 60/262,066
 PRIOR FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: US 09/722,329
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: US 09/262,109
 PRIOR FILING DATE: 1999-03-04
 PRIOR APPLICATION NUMBER: PCT/US98/18360
 PRIOR FILING DATE: 1998-09-03
 PRIOR APPLICATION NUMBER: US 09/722,329
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: US 09/262,109
 PRIOR FILING DATE: 1999-03-04
 PRIOR APPLICATION NUMBER: PCT/US98/18360
 PRIOR FILING DATE: 1998-09-03
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/057,626
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/057,663
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: PCT/US98/18360
 PRIOR FILING DATE: 1998-09-03
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/057,626
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/057,663
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/057,669
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/058,667
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,674
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,974
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,973
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,667
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,666
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,974
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,973
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,666
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/050,112
 PRIOR FILING DATE: 1998-06-22
 NUMBER OF SEQ ID NOS: 206
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 119
 LENGTH: 124

RESULT 6
 US-10-047-021-119
 Sequence 119, Application US/10047021
 Publication No. US20040002591A1
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 50 Human Secreted Proteins
 FILE REFERENCE: PZ016P2
 CURRENT APPLICATION NUMBER: US/10/047,021
 CURRENT FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: US 60/262,066
 PRIOR FILING DATE: 2001-01-18
 PRIOR APPLICATION NUMBER: US 09/722,329
 PRIOR FILING DATE: 2000-11-28
 PRIOR APPLICATION NUMBER: US 09/262,109
 PRIOR FILING DATE: 1999-03-04
 PRIOR APPLICATION NUMBER: PCT/US98/18360
 PRIOR FILING DATE: 1998-09-03
 PRIOR APPLICATION NUMBER: US 60/057,626
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/057,663
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: PCT/US98/18360
 PRIOR FILING DATE: 1998-09-03
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/057,669
 PRIOR FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 60/058,667
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,974
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,973
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,667
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/058,666
 PRIOR FILING DATE: 1997-09-12
 PRIOR APPLICATION NUMBER: US 60/050,112
 NUMBER OF SEQ ID NOS: 206
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 119
 LENGTH: 124

RESULT 7
 US-10-047-021-119
 Query Match 38.8%; Score 593; DB 15; Length 124;
 Best Local Similarity 98.3%; Pred. No. 2.6e-53; Mismatches 0; Indels 0; Gaps 0;
 Matches 113; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 NAME/KEY: SITE
 LOCATION: (75)
 OTHER INFORMATION: Xaa equals any amino acid
 OTHER INFORMATION: Xaa equals any amino acid
 SEQ ID NO 119
 LENGTH: 124

TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE: SITE
 NAME/KEY: SITE
 LOCATION: (106)
 OTHER INFORMATION: Xaa equals any amino acid
 NAME/KEY: SITE

Db 1 MSPPGTGCSAGLMLTVGMLLGLQSARGTNTAVODAGLAHGEGERETENDSETAE 60
 QY 61 NYAPPEPTEVDNSRNRAVKEVERFGMCTTCGIGVRREVILNGCPGGSKCVRVAREC 115
 Db 61 NYAPSETEDVSNRNRAVKEVERFGMCTTCGIGVRREVILNGCPGGSKCVRVAREC 115

RESULT 7
 US-10-411-224-119
 ; Sequence 119, Application US/10411224
 ; Publication No. US2003016906A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 50 Human Secreted Proteins
 ; FILE REFERENCE: P2016P1
 ; CURRENT APPLICATION NUMBER: US/10/411,224
 ; CURRENT FILING DATE: 2003-04-11
 ; PRIOR APPLICATION NUMBER: US/09/722,329
 ; PRIOR FILING DATE: 2000-11-28
 ; PRIOR APPLICATION NUMBER: 09/262,109
 ; PRIOR FILING DATE: 1999-03-04
 ; PRIOR APPLICATION NUMBER: 60/057,626
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/057,663
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/057,669
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/058,667
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,974
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,973
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/058,666
 ; PRIOR FILING DATE: 1997-09-12
 ; PRIOR APPLICATION NUMBER: 60/050,112
 ; PRIOR FILING DATE: 1998-01-22
 ; NUMBER OF SEQ ID NOS: 206
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 119
 ; LENGTH: 125
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (75)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; FEATURES:
 ; NAME/KEY: SITE
 ; LOCATION: (125)
 ; OTHER INFORMATION: Xaa equals stop translation

US-10-411-224-119

Query Match 38 8%; Score 593; DB 14; Length 125;
 Best Local Similarity 98 3%; Pred. No. 2.6e-53; Indels 0; Gaps 0;
 Matches 113; Conservative 0; Mismatches 2;

QY 1 MSPRGTCGCSAGLMLTVGMLLGLQSARGTNTAVODAGLAHGEGERETENDSETAE 60
 Db 1 MSPRGTCGCSAGLMLTVGMLLGLQSARGTNTAVODAGLAHGEGERETENDSETAE 60

RESULT 8
 US-10-369-493-3346
 ; Sequence 116, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hinkle, Gregory J.

Db 58 TAENYAPPEPTEVDNSRNRAVKEVERFGMCTTCGIGVRREVILNGCPGGSKCVRVAREC 116
 QY 61 NYAPSETEDVSNRNRAVKEVERFGMCTTCGIGVRREVILNGCPGGSKCVRVAREC 115
 Db 61 NYAPSETEDVSNRNRAVKEVERFGMCTTCGIGVRREVILNGCPGGSKCVRVAREC 115

Query Match 67%; Score 103; DB 11; Length 255;
 Best Local Similarity 24.8%; Pred. No. 0.069; Indels 38; Gaps 8;
 Matches 41; Conservative 21; Mismatches 65; Indels 38; Gaps 8;

QY 59 TAENYAPPEPTEVDNSRNRAVKEVERFGMCTTCGIGVRREVILNGCPGGSKCVRVAREC 116
 Db 25 TPKTLAIPERLQRAVGKVI--INATCTVCGLGKESTCCEVGPDGVRKRCQTRRLC 82

; SEQ ID NO 538
; LENGTH: 255
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-737-538

Query Match 6.5%; Score 99; DB 14; Length 255;
Best Local Similarity 24.2%; Pred. No. 0.18; Mismatches 65; Indels 38; Gaps 8;
Matches 40; Conservative 22; Mismatches 65; Indels 38; Gaps 8;

Qy 58 TAEVYAPPENEDVSURRNVKEVERFEGMCTVCGIGSVR-EVILTEGCPGGSSKCVVRVECK 116
Db 25 TPKVLAIPBKLOAVGVVI--INAACTCTVCGAGSYKEETVCEVGPDGVRKCORLECL 82

Qy 117 GPTDGGW-----GKPIBSLSVRLAHTSPL---NRPKWKKLURQQSILIN 165
Db 83 TNWTCGMHLHFTLIGK-----PELSCUSSDILFGQDAFRPFWLR-----GVISID 131

Qy 166 DSATLEVRKESHPPLAFR-----CDT--LDNNETAVIKP 197
Db 132 DEVVKPFOANSHFWKFKYAOEYDSSTYRCDVQLVKNLVKRIV 176

Search completed: April 15, 2005, 14:18:51
Job time : 138 secs

Run on:	April 15, 2005, 14:04:21 ;	Search time 173 Seconds (without alignments)	Copyright (c) 1993 - 2005 Compugen Ltd.	
Om protein - protein search, using sw model				
Title:	US-10-809-655-9	6.5	255 6 ABR95755 Human sec	
Perfect score:	152B	2.5	255 6 ABR92974 Human sec	
Sequence:	MSPRGTCGSAQILMIVGHL.....LQDQFLPEMWGGDDASENNE 294	2.5	255 6 ABR90035 Human PRO	
Scoring table:	BLOSUM62	2.5	255 6 ABR68344 Novel hum	
Gapped:	10.0 , Gapext 0.5	3.0	255 6 ABR6397 Novel hum	
Searched:	2105692 seqs, 386760381 residues	3.1	255 6 ABR92828 Human sec	
Total number of hits satisfying chosen parameters:	2105692	3.2	255 6 ABR92828 Human sec	
Minimum DB seq length:	0	3.3	255 6 ABR08906 Novel hum	
Maximum DB seq length:	200000000	3.4	255 6 ABR02957 Novel hum	
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries				
Database :	A_Geneseq_16Dec04:*	3.5	255 6 ABR75111 Human sec	
1:	geneseqP1990B:*	3.5	255 6 ABR94873 Human sec	
2:	geneseqP1990B:*	3.5	255 6 ABR85846 Human PRO	
3:	geneseqP2000B:*	3.5	255 6 ABR99006 Novel hum	
4:	geneseqP2001B:*	3.5	255 6 ABR91927 Novel hum	
5:	geneseqP2002B:*	3.5	255 6 ABR9620 Human PRO	
6:	geneseqP2003as:*	3.5	255 6 ABR9641 Human sec	
7:	geneseqP2003bs:*	3.5	255 6 ABR67674 Human sec	
8:	geneseqP2004B:*	3.5	255 6 ABR80702 Human PRO	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES				
Result No.	Score	% Match	ALIGNMENTS	
		Length	DB ID	
			Description	
1	152B	100.0	294 4 AAB85346	RESULT 1
2	762.5	49.9	163 5 ABR62052	ID AAB85346 standard; protein; 294 AA.
3	762.5	49.9	163 5 ABR57229	XX
4	762.5	49.9	163 6 AD41111	AC AAB85346;
5	762.5	49.9	163 7 ADD37978	XX
6	593	38.8	124 5 ABR62056	DT 17-SEP-2001 (first entry)
7	593	38.8	124 6 AD45752	XX
8	593	38.8	124 6 AD41456	DE Sperm specific surface protein SAMP32.
9	593	38.8	124 7 ADD38087	XX
10	593	38.8	125 2 AAY12953	KW Sperm specific surface protein; C7/8; SAMP32; C58; contraceptive;
11	110	7.2	1315 8 ADM20693	XX
12	103	6.7	2 AAY31833	KW vaccine; antifertility; spermicide.
13	103	6.7	255 4 ABG02357	XX
14	103	6.7	255 5 AAR96170	OS Homo sapiens.
15	103	6.7	255 5 ABC64819	XX
16	103	6.7	255 8 ADI78086	PR WO200153352-A2.
17	102	6.7	1083 4 ABR61710	XX
18	99	6.5	255 4 AAB73684	PD 26-JUL-2001.
19	99	6.5	255 4 AAR29292	XX
20	99	6.5	255 5 AAR96195	PF 19-JAN-2001; 2000US-0176885P.
21	99	6.5	255 5 ABC64818	XX
22	99	6.5	255 6 ABU58668	PA (UVVI-) UNIV VIRGINIA PATENT FOUND.
23	99	6.5	255 6 ABU88216	PT Hao Z, Herr JC, Jayes FL, Shetty J, Wolkowicz MJ;
24	99	6.5	255 6 ABU84531	XX
25	99	6.5	255 6 ABR66405	PT DR N-PSDB; AAR22947.
			XX	
			PT New human sperm surface proteins C7/8, SAMP32 and C58 for development of contraceptive vaccines.	
			XX	
			PS Claim 10; Page 56-67; 63pp; English.	
			XX	
			CC The invention relates to novel human sperm specific surface proteins, C7/8, SAMP32 and C58. The proteins, nucleic acids encoding the sperm specific surface proteins and antibodies specific for the proteins are useful for making contraceptive compositions including contraceptive vaccines. The vaccines produced by the invention are hoped to be more effective than previous contraceptive vaccines which only caused 75% inhibition of fertility. The present sequence represents the human sperm specific surface protein SAMP32.	
			CC Sequence 294 AA;	
			SQ	
Query Match Best Local Similarity		100.0%; Score 1528; DB 4; Length 294;		

Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSPPGTGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

DB 1 MSPRTGEGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

OY 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

DB 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

OY 181 FRCPTLDNNEIVATKFTYTTSSILQMRSSLPADALIPTVLTGIVCIFPFLIFI 240

DB 181 FRCPTLDNNEIVATKFTYTTSSILQMRSSLPADALIPTVLTGIVCIFPFLIFI 240

OY 241 INWAAVKAFPGAKASTPEVOSBSSVRYDSDTSIDQLPTEMPRDALLEWEWE 294

DB 241 INWAAVKAFPGAKASTPEVOSBSSVRYDSDTSIDQLPTEMPRDALLEWEWE 294

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

OY 1 MSPPGTGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

DB 1 MSPRTGEGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

OY 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

DB 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 156

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 156

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 156

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 156

OY 1 MSPPGTGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

DB 1 MSPRTGEGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

OY 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

DB 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

OY 181 FRCPTLDNNEIVATKFTYTTSSILQMRSSLPADALIPTVLTGIVCIFPFLIFI 240

DB 181 FRCPTLDNNEIVATKFTYTTSSILQMRSSLPADALIPTVLTGIVCIFPFLIFI 240

OY 241 INWAAVKAFPGAKASTPEVOSBSSVRYDSDTSIDQLPTEMPRDALLEWEWE 294

DB 241 INWAAVKAFPGAKASTPEVOSBSSVRYDSDTSIDQLPTEMPRDALLEWEWE 294

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

OY 1 MSPPGTGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

DB 1 MSPRTGEGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

OY 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

DB 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 156

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 156

OY 181 FRCPTLDNNEIVATKFTYTTSSILQMRSSLPADALIPTVLTGIVCIFPFLIFI 240

DB 181 FRCPTLDNNEIVATKFTYTTSSILQMRSSLPADALIPTVLTGIVCIFPFLIFI 240

OY 241 INWAAVKAFPGAKASTPEVOSBSSVRYDSDTSIDQLPTEMPRDALLEWEWE 294

DB 241 INWAAVKAFPGAKASTPEVOSBSSVRYDSDTSIDQLPTEMPRDALLEWEWE 294

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

OY 1 MSPPGTGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

DB 1 MSPRTGEGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

OY 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

DB 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 180

OY 1 MSPPGTGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

DB 1 MSPRTGEGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

OY 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

DB 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing infections; (e) neurological diseases such as viral, bacterial, fungal and parasitic infections.

Sequence 163 AA;

Query Match 49.9%; Score 762.5; DB 5; Length 163;

Best Local Similarity 94.2%; Fred. No. 3.2e-74; Matches 147; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

OY 1 MSPPGTGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

DB 1 MSPRTGEGSAGLMTVGMLLAGQSARGNTVAVDAGLAHGERGERETENDSEPAE 60

OY 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

DB 61 NYAPPETEDVSNRNVKVEFGMCTVTCGIGVRVILTINGCPGGESKCVVRVBECRGPTD 120

OY 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 156

DB 121 CGMKPKTPIBSLESVRACHTSPLNPKMMKLIRQDODSILNLDSALLEVREKSHPLA 156

New human secreted polypeptides and polynucleotides, useful for diagnosing, treating or preventing e.g. immune disorders, inflammatory conditions, respiratory disorders, cancers, CNS disorders, or neurodegenerative disorders.

The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,

THE invention relates to novel genes (ABQ92553-ABQ92607) and proteins (ABP6013-ABP6153) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification.

The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,

XX
 CC The invention relates to 592 new human secreted polypeptides useful for
 CC diagnosing, treating or preventing e.g. immune disorders, inflammatory
 CC conditions, respiratory disorders, cancers, CNS disorders, or
 CC neurodegenerative disorders, or polypeptides comprising an amino acid
 CC sequence at least 95% identical to the new sequences. The polypeptides,
 CC antibodies or antibody fragments that bind to the polypeptides, nucleic
 acids encoding the polypeptides, agonists or antagonists that binds to
 the polypeptide, are useful in preparing diagnostic or pharmaceutical
 compositions for diagnosing, treating or preventing an e.g. immune
 CC disorders, inflammatory conditions (e.g. inflammatory bowel disease,
 CC nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
 CC allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
 CC (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
 CC disorders (e.g. Parkinson's disease or Alzheimer's disease), and
 CC cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
 CC polynucleotides are useful for chromosome identification, chromosome
 CC mapping, for controlling gene expression through triple helix formation
 CC or antisense DNA or RNA, in gene therapy, for identifying individuals
 CC from minute biological samples, in forensic biology, and as hybridization
 CC probes. The polypeptides are useful as molecular weight markers on
 CC sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
 CC gels, to raise antibodies, for testing biological activities, and for
 CC treating or preventing neural disorders, immune system disorders,
 CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
 CC renal, proliferative and/or cancerous diseases. This sequence corresponds
 CC to one of the polypeptide of the invention. Note: The sequence data for
 CC this patent did form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.
 XX

SQ Sequence 163 AA:

Query Match 49.9%; Score 762.5; DB 6; Length 163;
 Best Local Similarity 94.2%; Pred. No. 3.2e-74;
 Matches 147; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
 QY 1 MSPROTGCSAGLMLVGVWLLLAGIQLQSARGNTVTAQDAGLAHGEGERETENDSETAE 60
 Db 1 MSPROTGCSAGLMLVGVWLLLAGIQLQSARGNTVTAQDAGLAHGEGERETENDSETAE 60
 61 NYAPPETEDVSNRNVKEVERGMCTVTCGIVREVILTINGCPGGESKCVVRVERCRGPTD 120
 QY 61 NYAPPETEDVSNRNVKEVERGMCTVTCGIVREVILTINGCPGGESKCVVRVERCRGPTD 120
 Db 121 CGWGPKPISESLSVRLACHTSPNRFKMKWLRQ 156
 QY 121 CGWGPKPISESLSVRLACHTSPNRFKMKWLRQ 156
 Db 121 CGWGPKPISESLSVRLACHTSPNLFVSVIY-BELLQ 155
 XX

RESULT 4

AID4111 ADD4111 standard; protein; 163 AA.
 XX AC ADD4111;
 XX DT 20-NOV-2003 (first entry)
 XX DB Human secreted protein.
 XX KW Human; Secreted protein; cancer; hyperproliferative disorder;
 KW rheumatoid arthritis; autoimmune disorder; haemopoietic disorder;
 KW anaemia; allergic reaction; asthma; cardiovascular disorder;
 KW wound healing; cytosolic; immunosuppressive; nootropic; neuroprotective;
 KW antiviral; antiallergic; hepatotoxic; antiidiabetic; antiinflammatory;
 KW vulnerability; cardiac; gene therapy.
 XX OS Homo sapiens.
 XX PN WO2002102993-A2.
 XX PD 27-DEC-2002.

PF 19-MAR-2002; 2002WO-US008123.
 XX
 PR 21-MAR-2001; 2001US-027340P.
 PR 19-JUL-2001; 2001US-036171P.
 PR 13-NOV-2001; 2001US-0331287P.

XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Rosen CA, Ruben SM;
 XX DR WPI; 2003-175238/17.

XX PT New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing,
 PT preventing or treating cancer or other hyperproliferative disorder,
 PT asthma, allergies or AIDS.

XX PS Claim 1; SEQ ID NO 1493; 3205PP; English.

The invention relates to novel genes ADA39629-ADA40565 and proteins
 ADA40566-ADA1501 for human secreted proteins, useful for preventing,
 treating or ameliorating medical conditions e.g. by protein or gene
 therapy. The polypeptides, nucleic acid molecules, antibodies or their
 fragments, and agonists or antagonists that bind to the polypeptide are
 useful for preparing a diagnostic or pharmaceutical composition for
 diagnosing or treating cancer or other hyperproliferative disorder. The
 polypeptides and nucleic acid molecules are also useful for detecting,
 preventing, diagnosing, prognosticating, treating or ameliorating cancer
 or other hyperproliferative disorders including neoplasms, autoimmune
 disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
 erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
 anaemia), haematopoietic or haematological disorders (e.g. anaemia,
 thrombocytopenia), allergic reactions including asthma or eczema,
 inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 fungal or viral infections including HIV/AIDS), or wound healing and
 useful for chromosome identification, radiation hybrid mapping or long-
 range restriction mapping, as molecular weight markers, or as
 hybridization or diagnostic probes. The polypeptides and antibodies are
 useful for providing immunological probes for differential identification
 of the tissues immunohistochemistry assays. Note: The sequence data for
 this parent did not form part of the printed specification, but was
 obtained in electronic format directly from WIPO at
 CC ftp://wipo.int/pub/published_pct_sequences.

SQ Sequence 163 AA;

Query Match 49.9%; Score 762.5; DB 6; Length 163;
 Best Local Similarity 94.2%; Pred. No. 3.2e-74;
 Matches 147; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
 QY 1 MSPROTGCSAGLMLVGVWLLLAGIQLQSARGNTVTAQDAGLAHGEGERETENDSETAE 60
 Db 1 MSPROTGCSAGLMLVGVWLLLAGIQLQSARGNTVTAQDAGLAHGEGERETENDSETAE 60
 61 NYAPPETEDVSNRNVKEVERGMCTVTCGIVREVILTINGCPGGESKCVVRVERCRGPTD 120
 QY 61 NYAPPETEDVSNRNVKEVERGMCTVTCGIVREVILTINGCPGGESKCVVRVERCRGPTD 120
 Db 121 CGWGPKPISESLSVRLACHTSPNRFKMKWLRQ 156
 QY 121 CGWGPKPISESLSVRLACHTSPNLFVSVIY-BELLQ 155
 Db 121 CGWGPKPISESLSVRLACHTSPNLFVSVIY-BELLQ 155
 XX

RESULT 5

ADD7978 ID ADD37978 standard; protein; 163 AA.
 XX AC ADD37978;
 XX

DT 15-JAN-2004 (first entry)
 XX DB Human secreted protein #161.
 KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 KW Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic.
 KW Homo sapiens.
 OS XX
 PN WO20020526-A2.
 PD 14-NOV-2002.
 PR 19-MAR-2002; 2002WO-US008279.
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUN-2001; 2001US-0316171P.
 PR 13-NOV-2001; 2001US-031287P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Robert CA, Ruben SM;
 XX WPI; 2003-140218/13.
 DR New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders, or related immediate hypersensitivity disorders.
 PS Claim 1; SEQ ID NO 460; 1323pp; English.
 CC The present invention relates to an isolated polypeptide or human secreted protein. The polypeptides, nucleic acid molecules, antibodies or their fragments, and agonists or antagonists that bind are useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders. The polypeptide is also useful for identifying a binding partner by contacting the polypeptide with a binding partner, and determining whether the binding partner increases or decreases the activity of the polypeptide. The polypeptides and nucleic acid molecules are also useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating inflammatory disorders, neoplastic diseases, wound healing and disorders of epithelial cell proliferation, immune disorders, cardiovascular disorders, blood-related disorders, infectious diseases, endocrine disorders, or gastrointestinal disorders. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping, as molecular weight markers, or as hybridization and diagnostic probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The present sequence represents a human secreted protein.
 XX SQ Sequence 163 AA;
 Query Match Best Local Similarity 49.9%; Score 762.5; DB 7; Length 163;
 Matches 147; Conservative 2; Mismatches 6; Indels 1; Gaps 1;
 QY 1 MSPRTGCGAGLINTVGMLLAGIQSARGINVTAAVODAGLAHGGGERBERTNDSETAR 60
 DQ 1 MSPRTGCGAGLINTVGMLLAGIQSARGINVTAAVODAGLAHGGGERBERTNDSETAE 60
 QY 61 NYAPRPTEDVSNRNWKVEFGRGMCTVTCGIGVRVLTNGCPEGESKCVURVERGEPD 120
 DQ 61 NYAPRPTEDVSNRNWKVEFGRGMCTVTCGIGVRVLTNGCPEGESKCVURVERGEPD 120
 QY 121 CGWKSXPSLESVRLAICHTSPNPKMKLRLQ 156
 DQ 121 CGWKSXPSLESVRLAICHTSPNPKMKLRLQ 155

ABP62065
 ID ABP62065 standard; protein; 124 AA.
 XX
 AC ABP62065;
 XX DT 12-NOV-2002 (first entry)
 DB Human secreted protein SEQ ID NO 119.
 XX Human; nontropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; pulmonary; antiparkinsonian; antisickling; anti-anemic; antiarthritic; cancer; antihaematuric; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiluler; anticonvulsant; antifungal; antiparasitic; cardiot; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
 XX OS Homo sapiens.
 XX WO200257420-A2.
 XX PR 17-JAN-2002; 2002WO-US001109.
 XX DR 25-JUL-2002.
 XX PD 18-JAN-2001; 2001US-0262066P.
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PI Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen CA, Olsen H;
 PI Eber R, Brewer LA;
 XX WPI; 2002-559716/64.
 DR New Polynucleotides and polypeptides useful for diagnosing, prognosis, treating or preventing e.g. neurodegenerative, central nervous system, autoimmune, respiratory, reproductive, or inflammatory diseases or disorders.
 XX PT
 XX PS Claim 11; Page 754-755; 785pp; English.
 CC The invention relates to novel genes (AB092553-AB092607) and proteins (ABP62013-ABP6215) useful for preventing, creating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing and infections; (e) neurological diseases such as viral, bacterial, fungal and parasitic infections.
 CC SQ Sequence 124 AA;
 Query Match Best Local Similarity 98.3%; Score 593; DB 5; Length 124;
 Matches 113; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MSPRTGCGAGLINTVGMLLAGIQSARGINVTAAVODAGLAHGGGERBERTNDSETAE 60
 DQ 1 MSPRTGCGAGLINTVGMLLAGIQSARGINVTAAVODAGLAHGGGERBERTNDSETAE 60
 QY 61 NYAPRPTEDVSNRNWKVEFGRGMCTVTCGIGVRVLTNGCPEGESKCVURVERGEPD 120
 DQ 61 NYAPRPTEDVSNRNWKVEFGRGMCTVTCGIGVRVLTNGCPEGESKCVURVERGEPD 120
 QY 61 NYAPRPTEDVSNRNWKVEFGRGMCTVTCGIGVRVLTNGCPEGESKCVURVERGEPD 115
 DQ 61 NYAPRPTEDVSNRNWKVEFGRGMCTVTCGIGVRVLTNGCPEGESKCVURVERGEPD 115

ADA57562
ID ADA57562 standard; protein; 124 AA.
XX
AC
XX
DT 20-NOV-2003 (first entry)
DB Human secreted protein #512.
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cyrostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovacular; antiartiosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology.
XX Homo sapiens.
XX WO2002102994-A2.
XX
PD 27-DEC-2002.
PP 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX (HUMA-) HUMAN GENOME SCI. INC.
PA
PI Rosen CA, Ruben SM;
XX DR
XX N-PGDB; ADA56669.
PT New human secreted polypeptides and polynucleotides, useful for
PT diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT conditions, respiratory disorders, cancers, CNS disorders, or
PT neurodegenerative disorders.
XX Claim 13; SEQ ID NO 1755; 1754pp; English.
CC The invention relates to 592 new human secreted polypeptides useful for
diagnosing, treating or preventing e.g. immune disorders, inflammatory
conditions, respiratory disorders, cancers, CNS disorders, or
neurodegenerative disorders, or polypeptides comprising an amino acid
sequence at least 95% identical to the new sequences. The polypeptides,
antibodies or antibody fragments that bind to the polypeptides, nucleic
acids encoding the polypeptides, agonists or antagonists that binds to
the polypeptide, are useful in preparing diagnostic or pharmaceutical
compositions for diagnosing, treating or preventing an e.g. immune
disorders, inflammatory conditions (e.g. inflammatory bowel disease,
nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
(e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
disorders (e.g. Parkinson's disease or Alzheimer's disease), and
cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
polynucleotides are useful for chromosome identification, chromosome
mapping, for controlling gene expression through triple helix formation
or antisense DNA or RNA, in gene therapy, for identifying individuals
from minute biological samples, in forensic biology, and as hybridization
probes. The polypeptides are useful for as molecular weight markers on
sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
gels to raise antibodies, for testing biological activities, and for
treating or preventing neural disorders, immune system disorders,
muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
renal, proliferative and/or cancerous diseases. This sequence corresponds
to one of the polypeptide of the invention. Note: The sequence data for
this patent did form part of the printed specification, but was obtained
in electronic format directly from WIPO at

CC ftp://wipo.int/pub/published_pct_sequences.
XX Sequence 124 AA;

Query	Match	Local Similarity	Score	DB	Length
MSPRGTGCSAGLMLTGWGLILAGHOSARGNVTAQDAGLAHRGEGERETENDSETAR	113	98.3%	593	6	124
MSPRGTGCSAGLMLTGWGLILAGLQSARGNTVAVODAGLAHRGEGERETENDSETAR	1	98.3%	601	6	124

Db 61 NYAPRTEDEVSNRNYKVEFGRMCTVTCGIVREVILNGCPGERSKCYTRVEC 115
61 NYAPRSETEDVSNRNYKVEFGRMCTVTCGIVREVILNGCPGEGESKCVVRVEC 115

RESULT 8
ADA41456
ID ADA41456 standard; protein; 124 AA.
XX
AC ADA41456;
XX
DT 20-NOV-2003 (first entry)
XX DE Human secreted protein.
XX KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haemopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cyrostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotoxic; antidiabetic; antiinflammatory;
KW vulnery; cardiant; gene therapy.
XX OS Homo sapiens.
XX PN WO2002102993-A2.
XX PD 27-DEC-2002.
XX PR 19-MAR-2002; 2002WO-US008123.
XX PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX PA (HUMA-) HUMAN GENOME SCI. INC.
XX PI Rosen CA, Ruben SM;
XX DR
XX WPI; 2003-175238/17.

PT New human secreted proteins and nucleic acid molecules, useful for
preparing a diagnostic or pharmaceutical composition for diagnosing,
preventing or treating cancer or other hyperproliferative disorder,
asthma, allergies or AINS.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
ADA0566-ADA41501 for human secreted proteins, useful for preventing,
treating or ameliorating medical conditions e.g. by protein or gene
therapy. The polypeptides, nucleic acid molecules, antibodies or their
fragments, and agonists or antagonists that bind to the polypeptide are
useful for preparing a diagnostic or pharmaceutical composition for
diagnosing or treating cancer or other hyperproliferative disorder. The
polypeptides and nucleic acid molecules are also useful for detecting,
preventing, diagnosing, prognosticating, treating or ameliorating cancer
or other hyperproliferative disorders including neoplasms, autoimmune
disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
anaemia), haematopoietic or hematological disorders (e.g. anaemia,
thrombocytopenia), allergic reactions including asthma or eczema,

CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
 CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
 CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
 CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
 CC fungal or viral infections including HIV/AIDS), or wound healing and
 CC disorders of epithelial cell proliferation. The nucleic acids are also
 CC useful for chromosome identification, radiation hybrid mapping or long-
 range restriction mapping, as molecular weight markers, or as
 hybridization or diagnostic probes. The polypeptides and antibodies are
 useful for providing immunological probes for differential identification
 of the tissues immunohistochemistry assays. Note: The sequence data for
 this patent did not form part of the printed specification, but was
 obtained in electronic format directly from WIPO at
 fpp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 124 AA;

Query Match 39.8%; Score 593; DB 6; Length 124;
 Best Local Similarity 98.3%; Pred. No. 6.1e-56; Matches 113; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSPRGTGCSAGLMLMTVGMLLAGIQLQSARGNTVTAQDAGLAHSGEGERETENDSETAE 60
 DB 1 MSPRGTGCSAGLMLMTVGMLLAGIQLQSARGNTVTAQDAGLAHSGEGERETENDSETAB 60
 OY 61 NYAPRPETEDVSNRNKVKEFVFGMCTVTCGIGVREVILTINGCPGGESKCVVRVSEC 115
 DB 61 NYAPSETEDVSNRNKVKEFVFGMCTVTCGIGVREVILTINGCPGGESKCVVRVSEC 115

RESULT 9

ID ADD38087 standard; protein; 124 AA.
 XX ID ADD38087
 AC AC
 XX DT 15-JAN-2004 (first entry)
 DB Human secreted protein #270.
 KW human secreted protein; Antiallergic; Antiinflammatory; Antibacterial;
 KW Ant-HIV; Cytostatic; Immunosuppressive; Hemostatic.
 KW Homo sapiens.
 PN WO200290526-A2.
 XX PD 14-NOV-2002.
 XX PP 19-MAR-2002; 2002WO-US008279.
 PR 21-MAR-2001; 2001US-0277340P.
 PR 19-JUL-2001; 2001US-0300171P.
 PR 13-NOV-2001; 2001US-0311287P.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM;
 XX DR WPI; 2003-140218/13.

XX New human secreted proteins and nucleic acid molecules, useful for
 PT preparing a diagnostic or pharmaceutical composition for diagnosing or
 PT treating allergic or asthmatic disorders, or related immediate
 PT hypersensitivity disorders.

Claim 1; SEQ ID NO 569; 1323pp; English.

XX The present invention relates to an isolated polypeptide or human
 CC secreted protein. The polypeptides, nucleic acid molecules, antibodies or
 CC their fragments, and agonists or antagonists that bind are useful for
 CC preparing a diagnostic or pharmaceutical composition for diagnosing or
 CC treating allergic or asthmatic disorders. The polypeptide is also useful

for identifying a binding partner by contacting the polypeptide with a

binding partner, and determining whether the binding partner increases or decreases the activity of the polypeptide. The polypeptides and nucleic acid molecules are also useful for detecting, preventing, diagnosing, prognosticating, treating or ameliorating inflammatory disorders

neoplastic diseases, wound healing and disorders of epithelial cell proliferation, immune disorders, cardiovascular disorders, blood-related disorders, infectious diseases, endocrine disorders, or gastrointestinal disorders. The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping, as molecular weight markers, or as hybridization or diagnostic probes. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The present sequence represents a human secreted protein.

XX SQ Sequence 124 AA;

Query Match 39.8%; Score 593; DB 7; Length 124;
 Best Local Similarity 98.3%; Pred. No. 6.1e-56; Matches 113; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSPRGTGCSAGLMLMTVGMLLAGIQLQSARGNTVTAQDAGLAHSGEGERETENDSETAE 60
 DB 1 MSPRGTGCSAGLMLMTVGMLLAGIQLQSARGNTVTAQDAGLAHSGEGERETENDSETAB 60
 OY 61 NYAPRPETEDVSNRNKVKEFVFGMCTVTCGIGVREVILTINGCPGGESKCVVRVSEC 115
 DB 61 NYAPSETEDVSNRNKVKEFVFGMCTVTCGIGVREVILTINGCPGGESKCVVRVSEC 115

RESULT 10

ID AAY12953 standard; protein; 125 AA.
 XX ID AAY12953
 AC AAY12953;
 XX DT 17-JUN-1999 (first entry)
 DB Amino acid sequence of a human secreted peptide.
 KW Human secreted protein; cancer; immune disorder; infection;
 KW inflammatory disorder; skin disorder; tumour; atherosclerosis;
 KW restenosia; autoimmune disorder; Alzheimer's disease;
 KW peripheral neuropathy; trauma; spinal cord injury; allergy;
 KW hematopoietic disorder; skeletal disorder; neurological disorder;
 KW arthritic disorder; asthma; immunodeficiency disease; AIDS;
 KW transplant rejection; SS.
 XX OS Homo sapiens.
 XX PH Location/Qualifiers
 PT Peptide 1..28 /note= "signal peptide"
 PT Protein 29..124 /note= "secreted protein"
 PT XX PN WO9911293-A1.
 XX DR 11-MAR-1999.
 XX PP 03-SEP-1998; 98WO-US018360.
 XX PR 05-SEP-1997; 97WOS-0057626P.
 PR 05-SEP-1997; 97WOS-0057663P.
 PR 05-SEP-1997; 97WOS-0057669P.
 PR 12-SEP-1997; 97WOS-0058666P.
 PR 12-SEP-1997; 97WOS-0058667P.
 PR 12-SEP-1997; 97WOS-0058973P.
 PR 12-SEP-1997; 97WOS-0058974P.
 PA (HUMA-) HUMAN GENOME SCI INC.

PI Moore PA, Ruben SM, Lafleur DW, Shi Y, Rosen GM, Olsen HS;
 PI Ebner R, Brewer LA;
 XK (CHEN X.)
 DR (GOLDMAN B S.)
 WPI; 1999-204988/17.
 DR N-PSDB, AAX51740.

PT New isolated human genes and the secreted polypeptides they encode - useful for diagnosis and treatment of e.g. neurological disorders, tumors, immune disorders, inflammation or hematological disorders.

XX Claim 11; Page 199; 215pp; English.

CC AAY12914-68 represent human secreted proteins. The polypeptides and their corresponding polynucleotides are useful for preventing, treating or ameliorating medical conditions, e.g. by protein or gene therapy.

CC Pathological conditions can also be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each polynucleotide, based on which tissues they are most highly expressed in, and include developing products for the diagnosis or treatment of cancer, immune disorders, infection, inflammatory disorders, skin disorders, tumours, atherosclerosis, restenosis, autoimmune disorders, Alzheimer's disease, peripheral neuropathies, trauma, spinal cord injuries, allergy, hematopoietic disorders, skeletal disorders, neurological disorders, arthritic disorders, asthma, immunodeficiency diseases, AIDS and transplant rejection. The polypeptides are also useful for identifying their binding partners

SQ Sequence 125 AA;

Query Match 38.8%; Score 593; DB 2; Length 125;
 Best Local Similarity 98.3%; Pred. No. 6.2e-56;
 Matches 113; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSPRPGCGSAGLMLMTWGLLJLAGLQSARGNTNTAAVODAGLAHEGGGBETENNSETAE 60
 Db 1 MSPRGCGSAGLMLMTWGLLJLAGLQSARGNTNTAAVODAGLAHEGGGBETENNSETAE 60
 OY 61 NYAPPETEDVSNRNVYKEVERGMCTVQIGIVREVLITNGCPGGESKCVVRVREC 115
 Db 61 NYAPPETEDVSNRNVYKEVERGMCTVQIGIVREVLITNGCPGGESKCVVRVREC 115

SQ Sequence 125 AA;

RESULT 11
 ADN20693 ID ADD20693 standard; protein; 1315 AA.

AC ADN20693;
 XX DT 02-DEC-2004 (first entry)
 DR Bacterial polypeptide #346.

KW Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polypeptide.

OS Bacteria.

XX US2003233675-A1.

PD 18-DEC-2003.

PP 20-FEB-2003; 2003US-00369493.

PR Z1-FEB-2002; 2002US-0360039P.

PA (CAOV/) CAO Y.
 (HINKL/) HINKLE G J.

PA (SLAT/) SLATER S C.
 PA (CHEN X.) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XK Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 DR WPI; 2004-061375/06.

PT New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 3346; 122pp; English.

CC The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by providing improved plant growth and development under at least one stress condition, improved lignin production or improved Galactomannan production. This sequence represents a bacterial polypeptide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1315 AA;

Query Match 7.2%; Score 110; DB 8; Length 1315;
 Best Local Similarity 25.2%; Pred. No. 0.005; Mismatches 93; Indels 50; Gaps 14;
 Matches 61; Conservative 38; Mismatches 93; Indels 50; Gaps 14;

OY 41 LAHEGERGERETENNSETAANYA--PPRPTEDV--SNRNWKVEFGMCTVQIGIVR 94
 Db 378 LAHEGERGERETENNSETAANYA--PPRPTEDV--SNRNWKVEFGMCTVQIGIVR 94
 OY 95 VILTNQCPGGES-KCVRVRECRGPTDCGW---GKPISESL--BSVRLACIHTSP-- 143
 Db 426 ---NNGAGBGSsGERFPTDQHLDVDDPVGGSSKKAKTSKESN----- 425
 OY 144 LNRFKTMWKL--RQDQSTILVNDSAILEVFKRSHPFLAFECDTDNNEVTA---TIRK 197
 Db 481 UNFPFTLLEPLSPRDVMGSAYNPREGDVK--AAPLSID-NIWANTVIASTTLAV 537
 OY 198 TWWTSBLQRSSLPATDALIF--VLTIGVICVRIPFLPILLIWAFAKFWGAK 254
 Db 538 IVYTGQTREALSTSPPSRSTGLEYEINSLTKIC---FLTFPLSIVVALSGFSTAK 593
 OY 255 AS 256
 Db 594 GN 595

RESULT 12
 AAY31833
 ID AAY31833 standard; protein; 255 AA.

XX AC AAY31833;
 XK DT 06-DEC-1999 (first entry)

Db	Qy	58 TAENYAPPETEVDISNRNTVKEVERGMCWTCIGIGVR-EVILATNGCPGGERSKCVVRVEBCR	83 TNWICGMHFTLIGK-----EPFSLCLSDILEFGOBAFRTWRLAR---GVSTD 131
Db	Qy	117 GPTDCGW-----GKPSBSLSVRVLACIHSPL--NRKTMWKLRQDQSQILVN 165	166 DSAILEVKRESHPLAFA-----CDT--LDNNEVATVKEP 197
Db	Qy	83 TNWICGMHFTLIGK-----EPFSLCLSDILEFGOBAFRTWRLAR---GVSTD 131	132 DEVFKPFOANSHVFKVQAQEVDSGTYRCDDVQVNLALVKRUYF 176
Db	Qy	166 DSAILEVKRESHPLAFA-----CDT--LDNNEVATVKEP 197	166 DSAILEVKRESHPLAFA-----CDT--LDNNEVATVKEP 197
Db	Qy	132 DEVFKPFOANSHVFKVQAQEVDSGTYRCDDVQVNLALVKRUYF 176	132 DEVFKPFOANSHVFKVQAQEVDSGTYRCDDVQVNLALVKRUYF 176
XX	XX	Human secreted protein, SEQ ID No 72.	Human secreted protein, SEQ ID No 72.
KW	KW	Human; secreted protein; autoimmune disease; rheumatoid arthritis;	Human; secreted protein; autoimmune disease; rheumatoid arthritis;
KW	KW	hyperproliferative disorder; neoplasm; breast; liver; ischaemia;	hyperproliferative disorder; neoplasm; breast; liver; ischaemia;
KW	KW	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;	cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW	KW	angiogenesis; nervous system disorder; Alzheimer's disease; infection;	angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW	KW	corneal infection; wound healing; ocular disorder; skin aging; sunburn;	corneal infection; wound healing; ocular disorder; skin aging; sunburn;
KW	KW	epithelial cell proliferation; organ transplantation; food additive;	epithelial cell proliferation; organ transplantation; food additive;
XX	XX	food storage.	food storage.
OS	OS	Homo sapiens.	Homo sapiens.
XX	XX	WO2010224721-A1.	WO2010224721-A1.
PD	PD	28-MAR-2002.	28-MAR-2002.
PR	PR	09-JAN-2001; 2001WO-US000544.	09-JAN-2001; 2001WO-US000544.
PR	PR	20-SEP-2000; 2000US-0234211P.	20-SEP-2000; 2000US-0234211P.
PA	PA	(HUMA-) HUMAN GENOME SCI INC.	(HUMA-) HUMAN GENOME SCI INC.
DR	DR	N-PSDB; ABIG69091.	N-PSDB; ABIG69091.
XX	XX	Isolated nucleic acid molecule encoding a human secreted protein is used	Isolated nucleic acid molecule encoding a human secreted protein is used
PT	PT	in preventing, treating or ameliorating a medical condition.	in preventing, treating or ameliorating a medical condition.
XX	XX	Claim 11; Page 498-499; 562pp; English.	Claim 11; Page 498-499; 562pp; English.
PS	PS		
XX	XX	The invention relates to an isolated nucleic acid molecule (I) encoding a	The invention relates to an isolated nucleic acid molecule (I) encoding a
CC	CC	human secreted protein (II), (I) and (II) are used to prevent, treat or	human secreted protein (II), (I) and (II) are used to prevent, treat or
CC	CC	ameliorate a medical condition in e.g. humans, mice, rabbits, goats,	ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC	CC	horses, cats, dogs, chickens or sheep. (I) and (II) are also used in	horses, cats, dogs, chickens or sheep. (I) and (II) are also used in
CC	CC	diagnosing a pathological condition or susceptibility to a pathological	diagnosing a pathological condition or susceptibility to a pathological
CC	CC	condition. The antibodies to (II) can also be used in alleviating	condition. The antibodies to (II) can also be used in alleviating
CC	CC	symptoms associated with the disorders and in diagnostic immunoassays	symptoms associated with the disorders and in diagnostic immunoassays
CC	CC	e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA).	e.g. radioimmunoassays or enzyme linked immunosorbent assays (ELISA).
CC	CC	Disorders which are diagnosed or treated include autoimmune diseases e.g.	Disorders which are diagnosed or treated include autoimmune diseases e.g.
CC	CC	rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the	rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the
CC	CC	breast or liver, cardiovascular disorders e.g. cardiac arrest,	breast or liver, cardiovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous
CC	CC	cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous	cerebrovascular disorders e.g. Alzheimer's disease, infections caused by bacteria,
CC	CC	viruses and fungi and ocular disorders e.g. corneal infection. The	CC
CC	CC	polypeptides can also be used to aid wound healing and epithelial cell	CC
CC	CC	proliferation, to prevent skin aging due to sunburn, to maintain organs	CC
CC	CC	before transplantation, for supporting cell culture of primary tissues,	CC
CC	CC	to regenerate tissues and in chemotaxis. The polypeptides can also be	CC
CC	CC	used as a food additive or preservative to increase or decrease storage	CC
CC	CC	capabilities. AAU96165-AAU96237 represent human secreted protein	CC
CC	CC	sequences and related sequences used in expression of the secreted	CC
CC	CC	proteins as described in examples of the invention.	CC
QQ	QQ	Sequence 255 AA;	Sequence 255 AA;

CC ABG63326-ABG65518 represent albumin fusion proteins of the invention
XX SQ Sequence 255 AA;

	Best Local Similarity	Pred. No.	Worst "Local" Similarity	Score	Length	Matches
QY	24.87	0.0422	20.77	2.02	203	41; Conservative
Db	21	65	21	0.0422	203	Mismatches
Qy	38	38	38	0.0422	203	Indels
Db	8	8	8	0.0422	203	Gaps
Qy	116	116	116	0.0422	203	TAEINYADPETYEDVSNRNVKEVERGMCCTVGIGWR-EVILNTNGCGPGESKCVVRVEECR
Db	82	82	82	0.0422	203	TPKTLALIPBKLUQBAGVKYI-INAATCTCTVTCGLSYKEEIVCEVGEPPGVRKQCOTRILC
Qy	165	165	165	0.0422	203	GPTDGCW-----GKPISESLSVRLAICHTSPL---NRPKOMWKLUARODDOSILVN
Db	131	131	131	0.0422	203	TNWICGMHLFTILIGK-----BFLSCUSSDTIEFGOBAFRFWILRAR-----GVISSTD
Qy	197	197	197	0.0422	203	DSAILETRAKESHPLAF-----CDT-LDNNEVATIVE
Db	176	176	176	0.0422	203	DSVFKPQFQANSHTWPKVIAQEYDVSGSTYRCVQDVLQTKNLRUKRUF
Qy	176	176	176	0.0422	203	DEVFKPQFQANSHTWPKVIAQEYDVSGSTYRCVQDVLQTKNLRUKRUF

Search completed: April 15, 2005, 14:11:58
Job time : 175 secs

OY 134 VRULACIHTSPNLRPKYMMKLLRQDQOSILVNDSAILEVRKESHLAFFECTLUNNETVA 193
 Db 671 VEQTC-----SROQSS-----REQRQPDPPLPPEV----- 698

OY 194 TIKTIVWYTTSBLONR----RSSPATDALIFLTVIGVILCIVTIPFLIPINWAAVK 248
 Db 699 -----EVBRKLRAGLASHIPEVLAGLISCHI-----IAIIFGIVFLFLHRCSPF 741

OY 249 AFPGKACASTPEVQBSQSYKOSTSLDQPLPTMPGEDALESENE 294
 Db 742 SFRQKVVT----MDRGLISYKG-----LPPE-----ANQB 768

RESULT 5
 S12783 40 antigen precursor - rat
 N;Alternate names: nerve growth factor receptor homolog
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: S12783; S08036
 R;Mallett, S.; Rosam, S.; Barclay, A.N.
 EMBO J. 9, 1063-1068, 1990.

A;Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
 A;Reference number: S12783; MUID:90214614; PMID:215791
 A;Accession: S12783
 A;Molecule type: mRNA
 A;Residues: 1-271 <MAL>
 A;Cross-references: UNIPROT:P15725; EMBL:X17037; NID:957830; PIDN:CA34897.1; PID:957831

C;Superfamily: CD27 antigen; NGF receptor repeat homology
 C;Keywords: growth factor receptor; transmembrane protein
 F1-19/Domain: signal sequence #status predicted <SIG>
 P1-20-271/Product: OX40 antigen #status predicted <MAT>
 P1-211-235/Domain: transmembrane #status predicted <TM>

Query Match 5.7%; Score 86.5; DB 2; Length 271;
 Best Local Similarity 21.1%; Pred. No. 7; Mismatches 69; Indels 53; Gaps 10;
 Matches 42; Conservative 35; MisMatches 69; InDelS 53; Gaps 10;
 Qy .99 NGCGGEGSKCVRRECRAFPDCGKGPKPSESLSVRLACI----HPSPLNPKYMK 152
 Db 93 NCTPTEBDTVC----OCRPGT----OPROPSHSKKGVDPCPGHFSPGSNACKPN- 141
 Qy 153 LIRQDQOSITLVNDSAILERKESHLAFLRCDTL-DNNETVATKE----TVVTS 202
 Db 142 -----TNTCLASQKQINHPASNLDTCEDRSLATLWETORTTFFRTVTS 188
 Qy 203 SELQMRSSLPATDA-----ALIFVLTIGVTCVFTIFLIFITIINWAA---VKAP 250
 Db 189 TTVPVPRITSOLPSTPITIVAPRGPAFAVILGIGLILAPITVLLAYLIRKAWRSNTPKFC 248
 Qy 251 WGAKASTPVEQSVBSSVRY 269
 Db 249 WGNSPRRTP-TQEEDQDTHF 266

Best Local Similarity 30.5%; Pred. No. 13; Matches 25; Conservative 8; Mismatches 28; Indels 21; Gaps 2;
 Db 22 AGLOSSARGINNTAVQDAGLAIHEGERGERETENDSETARYAPRETEDVSNRNVKE-- 78
 Qy 244 AGQQAGENANNAKKAEDGGAGNAGGQGQNNEGANA-----PNEKSVKYID 292
 Db 79 -----VEFGMCVTCGIGVGR 93
 Qy 293 KVRAVGVIEWTPCSVTCGVGVR 314

RESULT 7
 OZ20AL
 circumsporozoite protein precursor - Plasmodium cynomolgi (strain London)
 N;Alternate name: major sporozoite surface antigen
 C;Species: Plasmodium cynomolgi
 C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
 C;Accession: A26285
 R;Galinski, M.R.; Arnott, D.B.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Brea, V
 Cell 48, 311-319, 1987
 A;Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
 A;Reference number: A90889; MUID:87102878; PMID:3802196
 A;Accession: A26285
 A;Molecule type: DNA
 A;Residues: 1-378 <GAL>
 C;Comment: There are three distinct regions in the mature circumsporozoite protein, the apical membrane-anchoring sequence.
 C;Comment: There are 19 tandem copies of a 6-residue repeat and 6 copies of an 11-residue C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
 C;Keywords: sporozoite; surface antigen; tandem repeat
 F1-19/Domain: signal sequence #status predicted <SIG>
 P1-0-378/Product: circumsporozoite protein #status predicted <MAT>
 P1-88-211/Region: 6-residue repeats
 P1-212-277/Region: 11-residue repeats
 P1-303-336/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 5.6%; Score 85; DB 1; Length 378;
 Best Local Similarity 29.7%; Pred. No. 15; Mismatches 38; Conservative 11; MisMatches 51; Indels 28; Gaps 4;
 Matches 38; Conservative 11; MisMatches 51; Indels 28; Gaps 4;
 Qy 22 AGLOSSARGINNTAVQDAGLAIHEGERGERETENDSETARYAPRETEDVSNRNVKE-- 78
 Db 259 AGGGAGAGQAGGAGAGAGAGQ-----QNN-----EGANNPNAKLVKEYID 303
 Qy 79 -----VEFGMCVTCGIG-----REVLTINGPGGEGSKCVRVEECRGPPTCGWGKPLS 128
 Db 304 KIRSTGVWVSPCSVTCGKVRMERKVNANKKPEELDVNDLENVCTMDKCAIGPNTVS 363
 Qy 129 ESLESVRL 136
 Db 364 NSLGIVIL 371

RESULT 8
 C41156

circumsporozoite protein - Plasmodium vivax (isolate B7-4)

C;Species: Plasmodium vivax

C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

C;Accession: C41156

R;Oori, S.H.; Goldman, I.P.; Povoia, M.M.; Oliveira, S.; Alpers, M.P.; Lal, A.A.
 J. Biol. Chem. 266, 16297-16300, 1991
 A;Title: Wide distribution of the variant form of the human malaria parasite Plasmodium
 A;Reference number: A41156; MUID:91358402; PMID:1885563
 A;Accession: C41156
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-367 <ARN>
 A;Cross-references: UNIPROT:Q26169; GB:M20670; GB:J04090; NID:916013; PIDN:AA29534.1;
 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <THR1>
 P1-292-345/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 5.5%; Score 84.5; DB 2; Length 387;

Best local similarity 31.4%; Pred. No. 17; Mismatches 51; Indels 17; Gaps 5;
 Matches 38; Conservative 15; Mismatches 51; Indels 17; Gaps 5;

Qy 22 AGSQARGNTVTAQDAGLAHGERGEREETTENDSETAENYAPPETEDVSNRNVKE-- 78
 Db 271 AGQQRAGG--NIAINKKAGDAGAQG---ONNEGAN---APNEKSVIYEDWKRATV 319

Qy 79 VEGGMCTWTCGIGW--KEVILTMGGCPGESESKCCTVVRVBRCRGPTDCGNGKPISSESLSVR 135
 Db 320 TSWTPCSVTGUVGSVVRVRAVNTKKPEDLTNDLQSTDVTDMDKGAGIFNVVNSLGLV 379

Qy 136 L 136
 Db 380 L 380

RESULT 9
 Circumsporozoite protein - Plasmodium vivax (isolate P19/D)
 C;Species: Plasmodium vivax
 C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004
 C;Accession: A41156
 R;Qard, S.H.; Goldman, I.P.; Povoao, M.M.; Oliveira, S.; Alpers, M.P.; Lal, A.A.
 J; Biol. Chem. 266, 16297-16300, 1991
 A;Title: Wide distribution of the variant form of the human malaria parasite Plasmodium
 A;Reference number: A41156; MUID:91358402; PMID:1885563

A;Accession: A41156
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-395 <QAR>
 A;Cross-references: UNIPROT:Q7M3X0; GB:M69059
 C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
 P;320-373/domain: thrombospondin type 1 repeat homology <THIR1>

Query Match
 Best Local Similarity 5.5%; Score 84; DB 2; Length 395;
 Matches 28; Conservative 9; Mismatches 17; Indels 28; Gaps 4;

Qy 22 AGIQSARGINTVTAQDAGLAHGERGEREETTENDSETAENYAPPETEDVSNRNVKE-- 78
 Db 279 AGQQAGG--NIAINKKAGDAGAQG---ONNEGANA-----TNEKSVKBYD 320

Qy 79 -----VEFGMCTWTCGIGVR 93
 Db 321 KVRAAVGNEWTPCSVTGUVGR 342

RESULT 10
 SLP(w7) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_change 09-Jul-2004
 C;Accession: I48771
 R;Hemerway, C.; Kalf, M.; Stavenhagen, J.; Watthall, D.; Robins, D.
 Nucleic Acids Res 14, 2539-2554, 1986
 A;Title: Sequence comparison of alleles of the fourth component of complement (C4) and a
 A;Reference number: I48274; MUID:86176748; PMID:3008092

A;Accession: I48771
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-594 <RES>
 A;Cross-references: UNIPROT:Q62238; EMBL:X06454; NID:954105; PIDN:CA29760.1; PID:954106
 C;Superfamily: alpha-2-macroglobulin

Query Match
 Best local similarity 22.9%; Score 84; DB 2; Length 594;
 Matches 50; Conservative 31; Mismatches 77; Indels 60; Gaps 11;

Qy 20 LIAGQOSANG-TNTTAQDAGLAH-EGSGREERETTENDSETAENYAPPETEDVSNRNVKE 77
 Db 340 LLSPFHALLGDLEKILTSLSDRYVSHFETDPGVHLYFD-----VPTRECIGFQASQ 392

RESULT 11
 T09988
 probable transcription termination factor - Mycobacterium leprae
 C;Species: Mycobacterium leprae
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T09988
 R;Robison, K.
 submitted to the EMBL Data Library, September 1994
 A;Reference number: Z16911
 A;Accession: T09988
 A;Status: translated from GB/EMBL/DDJB
 A;Residues: 1-610 <ROB>
 A;Cross-references: UNIPROT:P45835; EMBL:U15186; NID:9699323; PID:9699332
 C;Keywords: ATP; transcription termination

Query Match
 Best Local Similarity 5.5%; Score 83.5; DB 2; Length 610;
 Matches 60; Conservative 30; Mismatches 102; Indels 57; Gaps 14;

Qy 4 RGPGCSAGLMTWGWL--LLAGLOSSRG-TNTTAQDAGLAHEGRGEB-ETENNSET 58
 Db 50 RALLANQAGVKGTSQMRKSBLLIAIEBRCQGQANTSVNDGPSSRDHGGSATAISTEALAAQ 109

Qy 59 AENYAPPSTEDVSNRNVKEVERFGMCTWTCGIGREVIL-----TNGCPGGSKC 108

Db 110 RQNAIVAEVSRRRGASRRA-----VTAGSTABATESDCQGTADDTRTLOGGSD 163

Qy 109 VWRVEBCRGPTDGWKGPKISESLESRSVLACIHSPL-----NRFKMMWKLR 155

Db 164 -TKTEK-RGP-DGNDQOQVREQSSLQ-----PRGDDDGSRQRGRGRFRDRRR 213

Qy 156 QDQSIILVNDSAILEYKES-HPLAFRCTDUNNEIVATIKP-----TVTTSSLOMR 208

Db 214 GERS-----GDGAELRQLDDVVQPVAGILVDLNDYAFVRTSGYLAGPHDVVYSMSM-VR 267

Qy 209 RSSPATDA 217
 Db 268 KNGLRRGDA 276

RESULT 12
 D75591
 probable cation transporter - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: D75591
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, B.K.; Peterson, J.D.; Dodson, R.J.; F
 , M.; Shen, M.; Yamashita, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Ventler, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: D75591
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-375 <WHI>
 A;Cross-references: UNIPROT:Q9RYF7; GB:AB001863; GB:AB001825; NID:96460670; PIDN:AAPI2426
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DRA0361

Mon Apr 18 12:47:49 2005

us-10-809-655-9.rpr

Page 6

Job time : 46 secs

GenCore version 5.1.6
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On protein - protein search, using sw model
Run on: April 15, 2005, 14:04:30 ; Search time 187 Seconds
(without alignments)

Title: US-10-809-655-9
Perfect score: 1528
Sequence: 1 MSPRGTCSSAGLMLTVGSHL.....LDQIPTENMPEGGEDDALSEWNE 294

Scoring table: BloSUM62
Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03;*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT	1
ID	Q9HBV2
AC	Q9HBV2;
DT	01-MAR-2001 (T=EMBL; 16, last sequence update)
DT	25-OCT-2004 (T=EMBL; 28, last annotation update)
DB	Sperm acrosome membrane protein SAMP32 (Sperm acrosome associated 1).
GN	Name=SAMP32; Synonyms=SPACAI;
OS	Homo sapiens (Human);
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Buteraria; Primates; Catarrhini; Hominidae; Homo.
RA	Hao Z., Wolkowicz M.J., Shetty J., Klotz K., Bolling L., Sen B., Westbrook V.A., Connor S., Flickinger C.J., Herr J.C.;
RA	LINE 21858310; PubMed=11870081;
RX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	LINE 21858310; PubMed=11870081;
RP	SEQUENCE FROM N.A.
RL	PROTEIN: P53234 (2002)
RL	SEQUENCE FROM N.A.
RC	TISSUE=TesBis;
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shulman C.M., Bhat N.K., Altschul S.F., Zeeberg B.R., Buetow K.H., Scheuer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Cabavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Garnicci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McElvaney P.J., McKernan K.J., Malek J.A., Gunnarsson P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Munnay D.M., Sodergren E.J., Lu X., Gibbe R.A., Fahey J., Helton E.B., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J.J., Schmitz J.J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalius D.E., Schnetich A., Schein J.E., Jones S.J., Marra M.A.;
RA	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RA	Proc Natl Acad Sci USA 99(16):9341-9346 (2002)
RA	DR: BC02488; AAC04881; -;
DR	Genew; HGNC:14967; SPACAI.

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	1528	100.0	294	Q9HBV2
2	1115.5	73.0	305	Q9HBV2
3	311	20.4	2	Q8YVM2
4	110	7.2	1331	2
5	104	6.8	1081	2
6	103	6.7	Q9HBV2	Q9HBV2
7	102	6.7	1093	2
8	100	6.7	Q9VNT0	Q9VNT0
9	99	314	2	Q8TRH5
10	99	6.5	255	2
11	99	6.5	628	2
12	97.5	6.4	Q9FCY5	Q9FCY5
13	97	6.3	KR11_SCHPO	Q9175
14	95	6.2	1014	2
15	95	6.2	Q9VQ99	Q9VQ99
16	94	6.2	1353	2
17	93.5	6.1	259	2
18	93	6.1	626	2
19	92.5	6.1	797	1
20	92	1949	2	F0JL1_BOVIN
21	91	6.0	401	1
22	91	6.0	1213	2
23	90.5	5.9	1003	2
24	90.5	5.9	1643	2
25	90.5	5.9	2179	2
26	90	5.9	Q9TB22	Q9TB22
27	89.5	5.9	Q9EGB8	Q9EGB8
28	89.5	5.9	Q7PXY6	Q7PXY6
29	89	800	2	Q00835
30	89	5.8	226	2
31	89	5.8	373	2
	5.8	378	1	CSP_PLAC1
				DR: P08675_Plasmidium

DR GO; GO:000803; P:growth factor activity; IEA.
 DR InterPro; IPR000762; PTN MK.
 SQ SEQUENCE FROM N.A.
 Query Match 100 %; Score 1528; DB 2; Length 294;
 Best local Similarity 100 %; Pred. No. 1:1e-122; Indels 0; Gaps 0;
 Matches 294; Conservative 0; Mismatches 0; InDelS 0; Gaps 0;
 RT prepare full-length cDNA libraries for rapid discovery of new genes. ";
 RL Genome Res 10:1617-1630(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=20530912; PubMed=10705861; DOI=10.1101/gr.152600;
 RA Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kondo H., Akiyama J., Nishi K., Kitsunai T., Toshiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujikawa S., Inoue K., Ogawa Y., Izawa M., Ohara E., Watanuki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 QY 61 NYAPPETEDVSNRNVKEVERGMCVTCGGIGVERVLTNGPGEKCVWVECRGPTD 120
 Db 61 NYAPPETEDVSNRNVKEVERGMCVTCGGIGVERVLTNGPGEKCVWVECRGPTD 120
 QY 121 CGWGKQISESLSRSVLACTHSPLNPKMKLRLDQOSITLVDNSAILEVKRKHPLA 180
 Db 121 CGWGKQISESLSRSVLACTHSPLNPKMKLRLDQOSITLVDNSAILEVKRKHPLA 180
 QY 181 FECTDLNNEVATIKFTVTTSSLQMRSSLPATDAILFVLTGIVCPIFLIFI 240
 Db 181 FECTDLNNEVATIKFTVTTSSLQMRSSLPATDAILFVLTGIVCPIFLIFI 240
 QY 241 LINWAIAKFAKGAKASTPEVOSSESSVRYKOSTSLDOLPTTEMPGEDDASEWN 294
 Db 241 LINWAIAKFAKGAKASTPEVOSSESSVRYKOSTSLDOLPTTEMPGEDDASEWN 294
 RESULT 2
 Q9DA48 PRELIMINARY; PRT; 305 AA.
 ID Q9DA48
 AC 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)
 DB Mus musculus adult male testis cDNA, RIKEN full-length enriched
 library, clone:1700011A02 product:weakly similar to SPERM ACROSOME
 GN NAME=4930540LO3R1;
 OS Mus musculus (Mouse);
 OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Buteraria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis; DOI=10.1016/S0076-6879(99)03004-9;
 RX MEDLINE=99277763; PubMed=0346336; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.,"
 RL Nature 420:563-573(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci P., Shibata Y., Hayashi N., Sugahara Y., Shibata K., Itoh M.,
 RA Kondo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RESULT 3
 Q80VM2 PRELIMINARY; PRT; 90 AA.
 ID Q80VM2
 AC 080VM2;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, last sequence update)
 RT 01-JUN-2003 (TREMBLrel. 24, last annotation update)

DR GO; GO:0007275; P:development; IBA.
 DR InterPro; IPR000183; Decarboxylase.
 DR InterPro; IPR000627; Dioxxygenase.
 DR InterPro; IPR003459; Pixin-like.
 DR InterPro; IPR002165; pixin_repeat.
 DR InterPro; IPR001627; Sema.
 DR InterPro; IPR000884; TSP1.
 DR InterPro; IPR000805; TSP1.
 DR Pfam; PF01437; PST; 1.
 DR Pfam; PF01403; Sema; 1.
 DR Pfam; PF00090; TSP1; 6.
 DR PRINTS; PRO105; TSP1 repeat.
 DR SMART; SM00123; PST; 1.
 DR SMART; SM00330; Sema; 1.
 DR SMART; SM00209; TSP1; 6.
 DR PROSITE; PS00879; ODR_DC_2_2; UNKNOWN_1.
 DR PROSITE; PS00092; TSP1; 6.
 DR PROSITE; PS00092; TSP1; 6.
 DR SEQUENCE; 1081 AA; 120435 MW; 561071C831C431D3 CRC54;
 DR SEQUENCE; 1081 AA; 120435 MW; 561071C831C431D3 CRC54;
 DR Query Match 6.8%; Score 104; DB 2; Length 1081;
 DR Best Local Similarity 22.1%; Pred. No. 7.2; Indels 80; Gaps 12;
 DR Matchers 62; Conservative 35; Mismatches 103; Indels 80; Gaps 12;
 DR
 DR Qy 43 HEGERBERGENNSETAENYAPPTEDVSNRNVKEVERG-----MCTVNGIGVR 93
 DR Db 806 HRGSGQ-----SRVCNNHACPABEQLSSNLNEVEHGWMSWSENACSVTVOGLER 859
 DR Qy 94 EVLTNGCGGG-----ESKC-VVREVECGPFDGKGWGPISSEASVYLAICHT 141
 DR Db 860 R-----PRTCLAGHDLCQGEALRKCEKCMPCNTGWS-AMSWSSSSDGIL--- 910
 DR Qy 142 SPLRKPKYMKLAKQDQSIITLVNDSALLEVRKSHPLAFCDTLDNNBIVATIKFTVVT 201
 DR Db 911 -----RHRCLVHQ-----PGSMCRCG-----AEFKTACY 936
 DR
 DR Qy 202 SSELOMRSSSLPATDAALFVLTIGVILCWEIILU-----PILINNAVAKFGKAASP 258
 DR Db 937 PNFBETBTOFASSTATLPIVIFVGLIFTVACLATYTRPKFEMLSAREALNKTTTASPD 996
 DR Qy 259 EVQEQSSVYKQDSTSOLPTE-----EMEGEDALESEN 293
 DR Db 997 TYPKQSSSLPTKD-YDOPRKROSSFRPAKTNLNGEN 1034
 DR
 DR Qy 7
 DR Db 970X67 PRELIMINARY; PRT; 255 AA.
 DR AC 06PTN7
 DR DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DR DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DR DE Similar to RAKEN cDNA 4930429020.
 DR GN Name=Loc388750;
 DR OS Homo sapiens (Human).
 DR OC Baktarya; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 DR OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 DR RN [1]
 DR RP SEQUENCE FROM N.A.
 DR RC TTSSR_Peripheral Nervous System;
 DR RX MEDLINE-22386257; PubMed=12479932; DOI=10.1073/pnas.242603899;
 DR RA Strausberg R.L., Feingold E.A., Grouse L.H., Degege J.G.,
 DR RA Klausner R.D., Collins F.S., Wagner L., Shuemann C.M., Schuler G.D.,
 DR RA Altacnul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
 DR RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
 DR RA Blatchko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 DR RA Stapleton M., Soares M.B., Bonaldo M.R., Cesavant T.L., Scheetz T.B.,
 DR RA Brownstein M.J., Usdin T.B., Tobiayuki S., Carninci P., Prange C.,
 DR RA Brownstein M.J., Usdin T.B., Tobiayuki S., Carninci P., Prange C.,
 DR RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guaratine P.H.,
 DR RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay J.J., Hulyk S.W.,
 DR RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 DR Fahy J., Heitman B., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 DR
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green R.D., Dickson M.C.,
 RA Grimmwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smialius D.E., Schneidt A., Schein J.B.,
 RA Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 DR [2]
 DR RN SEQUENCE FROM N.A.
 DR RC TISSUE_Peripheral Nervous System;
 DR RA Strausberg R., Submitted (Nov-2003) to the EMBL/GenBank/DDBJ databases.
 DR RL EMBL; BC061592; AAH61592.1.
 DR DR InterPro; IPR007110; Ig-like.
 DR DR PROSITE; PS00835; Ig_LIKE; 1.
 DR DR SEQUENCE; 255 AA; 28468 MW; 27FDBBE4FA76E021 CRC64;
 DR
 DR Query Match 6.7%; Score 103; DB 2; Length 255;
 DR Best Local Similarity 24.8%; Pred. No. 1.5; Indels 41; Mismatches 21; Gaps 38; Gaps 8;
 DR Matchers 41; Conservative 21; Mismatches 65; Indels 38; Gaps 8;
 DR
 DR Qy 58 TAENYAPPTEDVSNRNVKEVERG-----CPTGIGKETVCSVGPDGURKOTRRLC 116
 DR Db 25 TPKTAIPKEKLOBAVGKVIT-INATCIVTCGIGKETVCSVGPDGURKOTRRLC 82
 DR Qy 117 GPTDCGW-----GKPISESLESVRACIHSPL---NRFKYMKKLRRDQDQSIILVN 165
 DR Db 83 TNWICGMHLFTLIGK-----EFELSCSSLSDILEFGQBARFRTWRLAR---GVISTD 131
 DR Qy 166 DSALIEVRKSHLAP-----CDT-LDNNEBIVATIKP 197
 DR Db 132 DEVTKPFOANSHFWKFKVAQEVDGTVRCDDVOLVKNLRIVKRLYF 176
 DR
 DR Q7XU67 PRELIMINARY; PRT; 1091 AA.
 DR ID Q7XU67
 DR AC 07XU67;
 DR DT 01-OCT-2003 (Tremblrel. 25, Created)
 DR DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DR DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DR DE REG8041P.
 DR GN Name=Sema-5c;
 DR OS Drosophila melanogaster (Fruit fly).
 DR OC Baktarya; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 DR OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 DR OC Ephydriidae; Drosophilidae; Drosophila.
 DR NCBI_TaxID=7227;
 DR RN [1]
 DR RP SEQUENCE FROM N.A.
 DR RC STRAIN_Berkeley;
 DR RA Stapleton M., Brokabein P., Hong L., Agbayani A., Carlson J.,
 DR RA George R., Gonzalez M., Guerin H., Krommiller B., Farfan D., Frise E.,
 DR RA Champre M., Chavez C., Dorsett V., Dresenek D., Parfait D., Prisse E.,
 DR RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 DR RA Patel S., Phoumanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 DR RA Celniker S.;
 DR RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
 DR DR EMBL; BR009866; AAQ22435.1; -
 DR DR HSSP; Q92854; 101Z.
 DR DR FlyBase; FBgn028679; Sema-5c.
 DR DR GO; GO:0016020; C-membrane; IEA.
 DR GO; GO:0030324; P:catalytic activity; IEA.
 DR GO; GO:0008199; F:ferric iron binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006725; P:aromatic compound metabolism; IEA.
 DR DR GO; GO:002725; P:development; IEA.
 DR DR InterPro; IPR000833; Decarboxylase.
 DR DR InterPro; IPR000827; Dioxxygenase.
 DR DR InterPro; IPR003459; Pixin-like.
 DR DR InterPro; IPR002165; Pixin repeat.
 DR DR InterPro; IPR001627; Sema.

DR InterPro; IPR000894; TPBL.
 DR Pfam; PF01437; PSL; 1.
 DR Pfam; PF01403; Sema; 1.
 DR Pfam; PF0090; TSP1; 6.
 DR SMART; SM00423; PSL; 1.
 DR SMART; SM00600; Sema; 1.
 DR SMART; SM00209; TSP1; 6.
 DR PROSITE; PS00879; ODR DC 2_2; UNKNOWN_1.
 DR PROSITE; PS50092; TSP1; 6.
 SQ SQUENCE 1091 AA; 121681 MW; 2DPA873668BACF35 CRC64;
 Query Match 6.7%; Score 102; DB 2; Length 1091;
 Best Local Similarity 21.8%; Pred. No. 11; Mismatches 61; Conservative 37; MisMatches 102; Indels 80; Gaps 12;
 Matches 61; Conservative 37; MisMatches 102; Indels 80; Gaps 12;
 QV 43 HEGGRGBRERNDNSHAYNTAPPETEDVSNNVNVEFG-----MCTVTCGIGVR 93
 816 HRGRSQ-----SRVONIHCAPAREHQSSNSLNLNGEKGWSSEWSAGSVCIGLR 869
 Db 94 EULITNGCPCG-----BSKC-WVVERECGPTDGWKGKISLESVRLAICHT 141
 870 R--RPRRCILAGHDRLUCQRALEKQKCEMVCEDPLGS--AWSENNSCCSDGIRL---- 920
 QY 142 SPLNPKYKMKLRLDQDQSILVNDSAILEVKRSKPLAHCDTIANNEVATKFTV 201
 921 :-----RHRCLVEQ-----PGSMCGRG-----ABEFKTACV 945
 Db 202 SSEIQLMRRSSLPLATRALIYLTVLIGVTCVPIFLII--PITINWAAVKAFCWAKASTP 258
 947 PNECETQIASTATAPIVIGLFLVACCLATIERTKKPMLMSABEALNKTTTASFD 1006
 Db 259 EVQSEQSSSYKDSLQPT----EMPOGRDALSERN 293
 QY 1007 TYPNGYSSLPKD--YDOPRKQSSFRMPAKTSNLNGN 1044
 RN [2]
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RN MEDLINE=22426065; PubMed=12537568;
 RX Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodges A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacieb J.M., Park S., Preiffer B.D., Richards S., Sodergren E.J.,
 RA Svirska R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Shizuka S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RT Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12531753;
 RX Celinker S.E., Bergman C.M., Krommiller B., Carlson J., Svirska R.,
 RA Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Asburner M., Celinker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomic perspective."
 RT Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426079; PubMed=12531752;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Ruang Y., Kaminker J.S., Milburn G.H., Prochnik S.E.,
 RA Smith C.P., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamaoka C., Asburner M., Gellert W.M., Rubin G.M.,
 RA Lewis S.B.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review";
 RT Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RG FLYBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AED03542; AA49966.3; -.
 RG FLYBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 DR HSSP; P07996; IISL.
 DR Intact; Q9YVTO; -.
 DR PLYBase; FBgn028679; Sema-5C.
 DR GO; GO:0016020; C:Membrane; IEA.
 DR GO; GO:0003824; Fcatalytic activity; IEA.
 DR GO; GO:0008199; ferric iron binding; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006725; Paracrine compound metabolism; IEA.
 DR GO; GO:0007275; development; IEA.
 DR InterPro; IPR000183; Decarbonylase.
 DR InterPro; IPR006271; Dicoygenase.
 DR InterPro; IPR003659; Plexin-like.

DE	Invasion protein Ibea.
OS	<i>Escherichia coli</i> .
OC	Bacterium; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX	<i>Enterobacteriaceae</i> ; <i>Escherichia</i> .
RN	[1] NCBI_TaxID=562;
RN	SEQUENCE FROM N.A.
RP	SSOURCE FROM N.A.
RX	Medline=96029746; PubMed=591081;
RA	Ruang S.H., Wass C., Fu O., Prasadrao N.V., Stins M., Kim K.S.;
RT	"Escherichia coli invasion of brain microvascular endothelial cells in vitro and in vivo: molecular cloning and characterization of invasion gene lbe10.".
RT	Infect. Immun. 63:4470-4475(1995).
RN	[2]
RP	SEQUENCE FROM N.A.
RX	Medline=2045456; PubMed=1108113; DOI=10.1016/S1286-4579(00)01277-6;
RA	Ruang S.H., Stins M.F., Kim K.S.;
RT	"Bacterial penetration across the blood-brain barrier during the development of neonatal meningitis.".
RL	Microbes Infect. 2:1237-1244(2000).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	Medline=21136444; PubMed=11237732;
RA	Ruang S.H., Wan Z.S., Chen H.Y., Jong A.Y., Kim K.S.;
RT	"Further characterization of Escherichia coli brain microvascular endothelial cell invasion gene lbea by deletion, complementation, and protein expression.".
RT	J. Infect. Dis. 183:1071-1078(2001).
RN	[4]
RP	SEQUENCE FROM N.A.
RX	Medline=21652705; PubMed=11793250;
RA	Ruang S.H., Chen Y.H., Kong G., Chen S.H.M., Besemer J., Borodovsky M., Jong A.; "A novel genetic island of meningitic Escherichia coli K1 containing the ibea invasion gene (GmK): functional annotation and carbon-source-regulated invasion of human brain microvascular endothelial cells.".
RT	Funct. Integr. Genomics 1:312-322(2001).
DR	EMLB; AP289032; AAC93912; -.
DR	GO; GO:0016591; P:Oxidoreductase activity; IEA.
DR	GO; GO:0006118; P:Electron transport; IEA.
DR	InterPro; IPR000205; NAD BS.
DR	InterPro; IPR000103; Pyridine_redox_2.
DR	PRINTS; PR00469; FNDR0TASII;
SQ	SEQUENCE 456 AA; 49772 NW; 00FD72D7EB0B010 CRC64;
Query Match	Best Local Similarity 6.4%; Score 97.5; DB 2; Length 456;
Matches	53; Conservative 18.9%; 39; Mismatches 95; Indels 93; Gaps 10;
Qy	7 GCGAGLMLVGMILLAGLQSARGNTVNTAVODAGLAHEGEGBERTENNDSKARYAPPE 66
Db	49 GCGCAGMWTI-----AGVESIAWRHENTVEGSGLARIE-----ETAKSGMASS 92
Qy	67 TEVSNRNRWVKEVFGMC---TIVCGICIREV-----ILTNGCPGGEK 107
Db	93 PEPOSNSGAINBRFRKLVDAMVLEQAGYVRVIRITAVDVTKOQANLGLGVITESKGROI 152
Qy	108 CVRVEBGRGFTDCGW--GKPSSESLSVSRVLAG----- 138
Db	153 LANVIIDCTGDAIDAWFAGAFAPIKR-EERELMONTIVSCANINKATMQINSTEPKIG 211
Qy	139 -----IHTSPLNRFK-YMVKLRLQDQQTILVND-----SAILLEVRKES 176
Db	212 DWWGADEENKNWSYDVHRSQRDMPSYLGKVLRKERSAGTIPKVDTLGGSWSTTEYGDAN 271
Qy	177 HPLAFSCITLDNNNEIVATIKPTVTTSSLQMRSSLPATDA 217
Db	272 YLVVVSIPAVDCTMDVFD-----LTRABIEGKQAMQAIEA 306
RESULT 12	
ID	09FCY5
AC	09FCY5
DT	01-MAR-2001 (TREMBLel. 16, Created)
DT	01-MAR-2002 (TREMBLel. 20, Last sequence update)
DT	01-MAR-2004 (TREMBLel. 25, Last annotation update)
RESULT 13	KRP1_SCPO

ID	PRT; 709 AA.	DR	PIR; S51793; S51793.
Q09175;	01-NOV-1995 (Rel. 32, Created)	DR	HS3P; P31334; IOT5.
DT	01-NOV-1995 (Rel. 32, Last sequence update)	DR	MEROPS; S08-070; -.
DT	25-OCT-2004 (Rel. 45, Last annotation update)	DR	GeneDB; SP0C28E12-09c; -.
DB	Dibasic processing endoprotease precursor (EC 3.4.21.-) (KEX2-related protease).	DR	InterPro; IPR002009; Pept_S8_S53.
Name=kRP; Synonyms=kRP; ORFNames=SPAC22E12.09c;	DR	ProDom; P000717; Protidin.	
OS Schizosaccharomyces pombe (Fission yeast).	DR	PROSITE; PS00136; SUBTILASE_HIS; 1.	
OC Buletta; Rungl; Ascomyota; Schizosaccharomycetes;	DR	PROSITE; PS00138; SUBTILASE_SER; 1.	
OC Schizosaccharomyces.	DR	Calcium/Glycoprotein; Hydrolase; Serine protease; Signal;	
NCBI_TaxID=4866;	KW	Transmembrane; Zymogen.	
RN [1]	SEQUENCE FROM N.A.	FT SIGNAL	1 22 Potential.
RC STRAIN=EG545;	FT PROPEP	23 82 Potential.	
RC MEDLINE=95112801; PubMed=7813430;	FT CHAIN	103 102 Potential.	
RC Davey J., Davis K., Imai Y., Yamamoto M., Matthews G.;	FT DOMAIN	103 709 Dibasic processing endoprotease.	
RC "Isolation and characterization of kRP, a dibasic endopeptidase required for cell viability in the fission yeast Schizosaccharomyces pombe.";	FT DOMAIN	103 668 Luminal (Potential).	
RC STRAIN=972;	FT TRANSMEM	669 693 Potential.	
RC EMBO J. 13:5910-5921(1994).	FT DOMAIN	694 709 Cytoplasmic (Potential).	
RL [2]	FT ACT_SITE	152 152 Charge relay system (By similarity).	
RN SEQUENCE FROM N.A.	FT ACT_SITE	200 200 Charge relay system (By similarity).	
RC Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,	FT ACT_SITE	371 371 Charge relay system (By similarity).	
RA Taylor K., Taylor R.G., Rivey A., Walsh S.V., Warren T., Whitehead S.,	FT DISULFD	216 363 By similarity.	
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonpeze B.,	FT DISULFD	308 338 By similarity.	
RA Weltjens I., Vanstreels E., Rieger M., Schaefter M., Mueller-Auer S.,	FT CARBOHYD	155 155 Ser/Thr-rich.	
RA Gabel C., Fuchs M., Pritzl C., Holzer E., Moestl D., Hildebrand H., Reinhardt R., Pohl T.M.,	FT CARBOHYD	463 463 Charge relay system (By similarity).	
RA Borzym K., Langer I., Beck A., Lenach H., Reinhardt R., Pohl T.M.,	FT CARBOHYD	471 471 Charge relay system (By similarity).	
RA Egger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,	FT CARBOHYD	620 620 N-linked (GlycNAc. . .) (Potential).	
RA Goffeau A., Cadile B., Dreano S., Gloux S., Jelaure V., Mottier S.,	SQ SEQUENCE	709 AA; 70126 MW; 414FEBB99C9B0840 CRC64;	
RA Galibert F., Ayres S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,	Query Match	6.3%; Score 97; DB 1; Length 709;	
RA Lucas M., Rocheleau M., Gailardin C., Tallada V.A., Garzon A., Thode G.,	Best Local Similarity	25.8%; Pred. No. 17;	
RA Daga R.R., Cruzado L., Jimenez M., del Rey F., Benito J.,	Matches	Mismatches 52; Indels 46; Gaps 7;	
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,	QY	188 : :-----ATKFTVTTSELQMRSS-----LPATDAAL-IFVLTIGVI 228	
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,	Db	613 RPNSDLTNSSTLSPSISFTSIVSATPTSTSHIPPTVLPPTQPVLPSTREIVAP 672	
RA Sherbakovskiy G.V., Uszry D., Barrell B.G., Nurse P.,	QY	229 ICPLFLFLFLIPFILINWAQAKFAGAKASPEVSE 263	
RA "The genome sequence of Schizosaccharomyces pombe.";	Db	673 ITPLFLFAPIFPAVAVIWTWISAFWKAKAPPPLSQQE 707	
RL Nature 415:871-880(2002).	RESULT 14		
-> CC -> FUNCTION: Membrane-bound, subtilisin-like serine protease that processes the P-factor precursor and other precursor proteins.	Q9V9Q9		
-> CC -> ESSENTIAL FOR CELL VIABILITY.	Q9V9Q9	PRELIMINARY;	PRT; 1014 AA.
-> CC -> CATALYTIC ACTIVITY: Cleaves substrate on the C-terminal side of dibasic residues.	Q9V9Q9: 095833; DT 01-MAY-2002 (TREMBLrel. 13, Created)		
-> CC -> COFACTOR: Calcium.	DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)		
-> CC -> SUBCELLULAR LOCATION: Type I membrane protein. Late Golgi compartment (BY SIMILARITY).	DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)		
-> CC -> PTM: N-Glycosylated.	DB CG31619-PB (CGH19218p)		
-> CC -> SIMILARITY: Belongs to the peptidase S8 family. Furin subfamily.	GN Name=CG131; ORFName=CG31619;		
-> CC -> This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.ebi-sib.ch) or send an email to license@ebi-sib.ch).	OS Drosophila melanogaster (fruit fly).		
-> CC -> DR EMBL; X82435; CRA57818.1; -.	OC Drosophila; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oribatida; Endopterygota; Drosophilidae; Drosophila.		
-> CC -> RN [1]	RP SEQUENCE FROM N.A.		
-> CC -> MEDLINE=20196066; PubMed=1073132; DOI=10.1126/science.287.5461.2185; DR Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., DR Amatidis P.G., Scheerer S.R., Li P.W., Hoskins R.A., Galle R.P., DR George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., DR Sulston J.E., Worm M.J.R., Yandell M.D., Zhang Q., Chen L.X., DR Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D., DR			

FLyBase; Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

[7]

SEQUENCE FROM N.A.

STRAIN-Berkeley;

Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,

Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,

Nuno J., Peclib J., Paragas V., Park S., Phouanenavong S., Wan K.,

Yu C., Lewis S.B., Rubin G.M., Celniker S.;

Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.

EMBL: AB03731; AA57227; -;

EMBL: AV061825; AAL27636.1; -;

FlyBase; FBgn0051619; CG31619.

InterPro: IPR007110; Ig-like.

InterPro: IPR003558; Ig_C2.

InterPro: IPR000841; TSP1.

InterPro: IPR008085; TSP1.

InterPro: IPR00407; Ig_1.

InterPro: IPR00090; TSP1; Ig-like.

PRINTS: PRO1705; TSPIREPEAT.

SMART: SN00408; IgC2_1.

SMART; SN00219; TSP1; 8.

PROSITE; PS5092; Ig_LIKE; 1.

PROSITE; PS5092; TSP1; 6.

SEQUENCE; 1014 AA; 112440 MW; 030A1645935D5360 CRC64;

Query Match 6.2%; Score 95; DB 2; Length 1014;
Best Local Similarity 21.9%; Pred. No. 39; Gaps 14;
Matches 61; Conservative 33; Mismatches 88; Indels 96; Gaps 14;
Indel 74

QY 8 CSAGI-----IMTGWILLAGLGSARGITWTAQV-----DAGLAHEGEGBETENDSET 58

Db 419 CSTGTHCGGSLANKYGGTIGW--SSRSILHRSERKQHOLDSDADEDNEDENDENEGDDVDLIES 476

QY 59 AEN-----YA-----PPETEDVSNRN-----

Db 477 GÖDTDJDGEGLSIADOPPLYAHRTQRNQEAPDPRTMILMNGNSNNNFRGEDEBGRPS 536

QY 75 -----VVKKEYFGMCMVTCGIVGVRLITMGCP--GGESKCVVRVER--CRGPTDCGWGKPC 126

Db 537 LDPTYTKIKRNPNSPVSPTCIGIRR--RTYNKFLFBSYTVATVNDLSLGK-----KE 588

QY 127 ISSESLESVLACTHTS-----PLANRK-----YMKKLRLRQDQQSILVNDSAIL 170

Db 589 HDEVERVCVEDPCMPSHGFDDQFERRDSIKVGVSBRGKTYWR----BOCYTCSASCLQ 643

QY 171 EVRKESHPFLAFECDFLTNNNIVATIKFTVYTSSELQMR 208

Db 644 GVEE---LINCYREDNGRVVSPLCSPETKPRARV 677

RESULT 15
Q9V907 PRELIMINARY; PRT; 1353 AA.

ID Q9V907

AC Q9V907

DT Q9V907; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

GN CG31619-PA.

ORFname=CG31619;

Drosophila melanogaster (fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydriidae; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

RN [1]

SEQUENCE FROM N.A.

MBINB-22420679; PubMed=12537572;

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.J., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayrakoglu L., Beasley B.M., Beeson K.Y., Benos P.V., Bernan B.P., Bhanari D., Bolshakov S., Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Burtis K.C., Busam D.A., Butler H., Cadile E., Center A., Chandra I., Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Maya A.D., Dew I., Dietz S.M., Dodson K., Dup L.E., Downs M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Fesler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaser K., Globek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hobin D., Houston K.A., Howland T.J., Wei M.H., Ibewam C., Jalil M., Kalush P., Karpen G.H., Ke Z., Kenyon J.A., Ketchum K.A., Kimmel B.E., Kodira C.O., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levinsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mattie B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacleb J.M., Palazzolo M., Pettman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D., Scheeler P., Shen H., Shee B.C., Shend Kimos I., Simpson M., Skupski M.P., Smith T., Spier E., Spalding A.C., Stapleton M., Strong R., Sun E., Wang X., Wang Z.Y., Wasserman D.A., Weinrock G.M., Weissenbach J., Williams S.M., Woodageir, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yen R.F., Zaveri J.S., Zhang M., Zhang G., Zhao Q., Zheng L., Zhang X.H., Zhong P.N., Zhou W., Zhu S., Zhu X., Smith H.O., Zheba R.A., Myers B.W., Rubin J.C., Rubin G.M., "The genome sequence of *Drosophila melanogaster*,"; Science 287:2185-2195 (2000).

RN [2]

RN SEQUENCE FROM N.A.

RX MEDLINE-22420679; PubMed=12537568;

RA Celinker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champine M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Haverty T., Muzzny D.M., Nelson C.R., Park S., Peiffer B.D., Richards S., Soedergren E.J., Svartkas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M., "Finishing a whole genome shotgun: Release 3 of the *Drosophila melanogaster* euchromatic genome sequence,"; Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).

RN [3]

RN SEQUENCE FROM N.A.

RX MEDLINE-22420670; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Krommiller B., Carlton J., Svartkas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celinker S.E., "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomic perspective,"; Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).

RN [4]

RN SEQUENCE FROM N.A.

RX MEDLINE-22420679; PubMed=12537572;

RA Mikra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hrdlicky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Trup J.L., Whited B.J., Bayrakoglu L., Bernan B.P., Betencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Sru S.Q., Strobleton M., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.E., "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review,"; Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).

RN [5]

RN SEQUENCE FROM N.A.

RX MEDLINE-22420679; PubMed=12537572;

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gooley J.D., Amatadis P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.P., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

RN [6]

RN SEQUENCE FROM N.A.

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champé M., Pfeiffer B.D.,

RP War K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RG Abriel J.F., Agbayani A., An-H.J., Andrews-Pflanck C., Baldwin D.,

RL Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Breitler P.,

RA Burtsis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., May B.A.D., Dew I., Dietz S.M.,

RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fobler C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Iglesias C.,

RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Lai D., Lai Z.,

RA Lasko P., Let Y., Levitsky A.R., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattie B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosheroff A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nuskeen D.R., Pacielek J.M.,

RA Pallazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reiner K., Remington K., Saunders R.D., Scheeler P., Shen H.,

RA Shue B.C., Sjodin-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spierer B., Spadling A.C., Stapleton M., Strong R., Sun B.,

RA Starks R., Tector C., Turner C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstock M., Weissenbach J.,

RA Williams S.M., Woodager T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhiu X., Smith H.O.,

RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,

RT "the genome sequence of *Drosophila melanogaster*";

RT *Science* 287:185-2195 (2000).

[2] SEQUENCE FROM N.A.

RN RX MEDLINE=2242065; PubMed=12537563;

RA Celinker S.B., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

RA Pacluk J.M., Park S., Pfeiffer B.D., Richards S., Soergren R.J.,

RA Svartkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.B., Myers B.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*

RT melanogaster euchromatic genome sequence";

RT *Genome Biol.* 3:RESEARCH0079-RESEARCH0079 (2002).

[3] SEQUENCE FROM N.A.

RN RX MEDLINE=22420670; PubMed=12537573;

RA Kannicker J.S., Bergman C.M., Krommiller B., Carlson J., Svartkas R.,

RA Patel S., Frise B., Wheeler D.A., Lewis S.B., Rubin G.M.,

RA Ashburner M., Celinker S.B.,

RT "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomic perspective";

RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review";

RT Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).

SEQUENCE FROM N.A.

FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

RA War K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abriel J.F., Agbayani A., An-H.J., Andrews-Pflanck C., Baldwin D.,

RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Breitler P.,

RA Burtsis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., May B.A.D., Dew I., Dietz S.M.,

RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fobler C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Iglesias C.,

RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Lai D., Lai Z.,

RA Lasko P., Let Y., Levitsky A.R., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattie B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosheroff A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nuskeen D.R., Pacielek J.M.,

RA Pallazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reiner K., Remington K., Saunders R.D., Scheeler P., Shen H.,

RA Shue B.C., Sjodin-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spierer B., Spadling A.C., Stapleton M., Strong R., Sun B.,

RA Wang Z.Y., Wasserman D.A., Weinstock M., Weissenbach J.,

RA Williams S.M., Woodager T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhiu X., Smith H.O.,

RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,

RT "the genome sequence of *Drosophila melanogaster*";

RT *Science* 287:185-2195 (2000).

[2]

SEQUENCE FROM N.A.

RN RX MEDLINE=2242065; PubMed=12537563;

RA Celinker S.B., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

RA Pacluk J.M., Park S., Pfeiffer B.D., Richards S., Soergren R.J.,

RA Svartkas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.B., Myers B.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*

RT melanogaster euchromatic genome sequence";

RT *Genome Biol.* 3:RESEARCH0079-RESEARCH0079 (2002).

[3]

SEQUENCE FROM N.A.

RN RX MEDLINE=22420670; PubMed=12537573;

RA Kannicker J.S., Bergman C.M., Krommiller B., Carlson J., Svartkas R.,

RA Patel S., Frise B., Wheeler D.A., Lewis S.B., Rubin G.M.,

RA Ashburner M., Celinker S.B.,

RT "The transposable elements of the *Drosophila melanogaster* euchromatin: a genomic perspective";

RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review";

RT Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).

SEQUENCE FROM N.A.

FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.

RA War K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abriel J.F., Agbayani A., An-H.J., Andrews-Pflanck C., Baldwin D.,

RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley B.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Breitler P.,

RA Burtsis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., May B.A.D., Dew I., Dietz S.M.,

RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fobler C., Gabriellian A.B., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Iglesias C.,

RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.B., Kodira C.D., Kraft C., Kravitz S., Lai D., Lai Z.,

RA Lasko P., Let Y., Levitsky A.R., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattie B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milashina N.V., Mobarry C., Morris J., Mosheroff A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nuskeen D.R., Pacielek J.M.,

RA Pallazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reiner K., Remington K., Saunders R.D., Scheeler P., Shen H.,

RA Shue B.C., Sjodin-Klamos I., Simpson M., Skupski M.P., Smith T.,

RA Spierer B., Spadling A.C., Stapleton M., Strong R., Sun B.,

RA Wang Z.Y., Wasserman D.A., Weinstock M., Weissenbach J.,

RA Williams S.M., Woodager T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Smith H.O.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhiu X., Smith H.O.,

RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.,

RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*

RT melanogaster euchromatic genome sequence";

RT *Genome Biol.* 3:RESEARCH0079-RESEARCH0079 (2002).

[4]

SEQUENCE FROM N.A.

RN RX MEDLINE=2242069; PubMed=12537572;

RA Misra S., Crosby M.A., Mungall C.J., Matthew B.B., Campbell K.S.,

RA Headecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,

RA Smith C.D., Tupy J.L., Whitedfield E.J., Bayraktaroglu L., Berman B.P.,

RA Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,

RA Lewis S.B.;

RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review";

RT Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).

[5]

SEQUENCE FROM N.A.

RN RX FlyBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

[6]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 15, 2005, 14:08:19 ; Search time 22 Seconds
 Sequence: (without alignments)
 997.583 Million cell updates/sec

Title: US-10-809-655-9

Perfect score:

1 MSPRGTGCSAGLIMTVGMLI.....LDQQLPTEMPGEDDALESEWNE 294

Scoring table: BLASTM62
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:**

1: /cggn2_6/prodata/1/iaa/5A.COMB.pep:*

2: /cggn2_6/prodata/1/iaa/5B.COMB.pep:*

3: /cggn2_6/prodata/1/iaa/6A.COMB.pep:*

4: /cggn2_6/prodata/1/iaa/6B.COMB.pep:*

5: /cggn2_6/prodata/1/iaa/PCTUS.COMB.pep:*

6: /cggn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Length DB ID

Description

Matched 62; Conservative 36; Mismatches 102; Indels 80; Gaps 12;

Matches 62; Best Local Similarity 22.7%; Pred. No. 0.0085; DB 4; Length 479;

US-09-270-767-46823

Sequence 46823, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and Proteins of *Drosophila melanogaster*

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 46823

LENGTH: 479

TYPE: PRT

ORGANISM: *Drosophila melanogaster*

US-09-270-767-46823

RESULT 1

US-09-270-767-46823

Sequence 46823, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig et al.

TITLE OF INVENTION: Polymorphisms in Known Genes Associated

QY	43	HEGEGEBETENDSETAENTKAPPETEDVSNRANVKVEFG-----MCIVTVCIGVR	93
Db	204	HRRGSGQ-----SRVNCMACPABQESLNSDNEVERSGWCGSEWSACSVTCGLGR	257
QY	94	EVLITNGCPGG-----ESKG-VVRVEBRCGPTDCWGKPTESESLSVRACIHT	141
Db	258	R-RTRRCLASHDRQCGRALEQKCEMWPCDFLGS-----AWSWSSCSDGIRL--	308
QY	142	SPLNRFKMMKLUQDQHQSTILVNNSAILEVTKSHPLAFCDTLNNELVATIKTVWT	201
Db	309	-----RHRRECVO-----PGSHBCRG-----AEFKHACV	334
QY	202	SSBLQMRSSPATDAALIFLUTIGVILICPIFILLI--RIINWAIAKFWGAKASTP	258
Db	335	PNECETQTOASTATLIVPGFLGVLTWVACCLAYRTKPKRNLMSAREALKNTTTASED	394
QY	259	EVOSEGSRSVYKDSISLDQIPT-----EMPGEDDALESEWNE	293
Db	395	TYPNQISSLPKID--YDQRPKRQSSPRMPLKTSNLGN	432

RESULT 2

Sequence 6, Appli
 Sequence 9924, Appli
 Sequence 32, Appli
 Sequence 32, Appli
 Sequence 152, Appli
 Sequence 152, Appli
 Sequence 22, Appli
 Sequence 22, Appli
 Sequence 12643, Appli
 Sequence 2, Appli
 Sequence 20, Appli
 Sequence 20, Appli
 Sequence 6265, Appli
 Sequence 7397, Appli
 Sequence 2574, Appli
 Sequence 2, Appli
 Sequence 2620, Appli
 Sequence 363, Appli

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIORITY NUMBER: 60/241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 5981
LENGTH: 2181
TYPE: PRT
ORGANISM: Human
US-09-949-016-5981

Query Match Best Local Similarity 5.9%; Score 89.5; DB 4; Length 2181;
Matches 71; Conservative 21.2%; Pred. No. 6.1; Mismatches 97; Indels 121; Gaps 18;
QY 3.2 VTAIVAVODAGLAHGERGEBETENDSETAENYAPPETEDVSURNNVVERGNCITVCGIG 91
QY 3.2 VTAIVAVODAGLAHGERGEBETENDSETAENYAPPETEDVSURNNVVERGNCITVCGIG 91
Db 449 ITQA-EDIDPENEEREGESEKRTSMPTS---ESTESNTENSGEGE----- 491
Db 92 VREVILTINGCPG-----GESKCUVVRBECRGPTDC-GWGPKESESLESVR----- 135
Db 492 -----NRGGCGSLWCWWRRGAAKA-----GPSGCRWRGAISKSLSRRRWR 537
Qy 136 -----LACHTSPNREKRM---WKLIRD-QSSTILVNDSAI 170
Db 531 FNRRRCRAAVKSVTFTWLVLTFLNTLTSSEHYNPQDWLTQDIAKNTLALFTCEM 590
Qy 171 EVRKESHPL-----AFBC-----DTLDNNBEVATIKFVTVTYSBEL---QMR 208
Db 591 LVRKMSLGLQAYFVSLPNPFCPVCGGTTIELVBLNSPLGISVFCVRLIRPKV 650
Qy 209 R--SSPATDAHLI-FVLTIGVIVCFLILLIFLILINNAVAKFAGAKASTPEVQEQS 265
Db 651 RHWTSLSNLVSLNSMSKSIASLLLPLFLITFSLIG---MOLFGGKENFDOTKRS 706
Qy 266 SVRYKDSTSIDOLPTE-----MPGRDDAISERN 293
Db 714 -----TVDNFPOLLTVFOILTGD----WN 735
Db 598 LVRKMSLGLQAYFVSLPNPFCPVCGGTTIELVBLNSPLGISVFCVRLIRPKV 657
Db 538 FNRRRCRAAVKSVTFTWLVLTFLNTLTSSEHYNPQDWLTQDIAKNTLALFTCEM 597
Qy 171 EVRKESHPL-----AFBC-----DTLDNNBEVATIKFVTVTYSBEL---QMR 208
Db 658 RHWTSLSNLVSLNSMSKSIASLLLPLFLITFSLIG---MOLFGGKENFDOTKRS 713
Qy 266 SVRYKDSTSIDOLPTE-----MPGRDDAISERN 293
Db 714 -----TVDNFPOLLTVFOILTGD----WN 735

RESULT 3
US-09-949-016-8295
Sequence 8295, Application US/09949016
Patient No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISBASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: CURRENT APPLICATION NUMBER: US/09/949,016
TITLE OF INVENTION: CURRENT FILING DATE: 2000-04-14
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 8295
LENGTH: 2188
TYPE: PRT
ORGANISM: Human
US-09-949-016-8295

Query Match 5.9%; Score 89.5; DB 4; Length 2188;

Best Local Similarity 21.2%; Pred. No. 6.1;
Matches 71; Conservative 46; Mismatches 97; Indels 121; Gaps 18;
Qy 32 VTAIVAVODAGLAHGERGEBETENDSETAENYAPPETEDVSURNNVVERGNCITVCGIG 91
Db 449 ITQA-EDIDPENEEREGESEKRTSMPTS---ESTESNTENSGEGE----- 491
Db 92 VREVILTINGCPG-----GESKCUVVRBECRGPTDC-GWGPKESESLESVR----- 135
Db 492 -----NRGGCGSLWCWWRRGAAKA-----GPSGCRWRGAISKSLSRRRWR 537
Qy 136 -----LACHTSPNREKRM---WKLIRD-QSSTILVNDSAI 170
Db 531 FNRRRCRAAVKSVTFTWLVLTFLNTLTSSEHYNPQDWLTQDIAKNTLALFTCEM 590
Qy 171 EVRKESHPL-----AFBC-----DTLDNNBEVATIKFVTVTYSBEL---QMR 208
Db 591 LVRKMSLGLQAYFVSLPNPFCPVCGGTTIELVBLNSPLGISVFCVRLIRPKV 650
Qy 209 R--SSPATDAHLI-FVLTIGVIVCFLILLIFLILINNAVAKFAGAKASTPEVQEQS 265
Db 651 RHWTSLSNLVSLNSMSKSIASLLLPLFLITFSLIG---MOLFGGKENFDOTKRS 706
Qy 266 SVRYKDSTSIDOLPTE-----MPGRDDAISERN 293
Db 714 -----TVDNFPOLLTVFOILTGD----WN 735
Db 598 LVRKMSLGLQAYFVSLPNPFCPVCGGTTIELVBLNSPLGISVFCVRLIRPKV 657
Db 538 FNRRRCRAAVKSVTFTWLVLTFLNTLTSSEHYNPQDWLTQDIAKNTLALFTCEM 597
Qy 171 EVRKESHPL-----AFBC-----DTLDNNBEVATIKFVTVTYSBEL---QMR 208
Db 658 RHWTSLSNLVSLNSMSKSIASLLLPLFLITFSLIG---MOLFGGKENFDOTKRS 713
Qy 266 SVRYKDSTSIDOLPTE-----MPGRDDAISERN 293
Db 714 -----TVDNFPOLLTVFOILTGD----WN 735

RESULT 4-736-2
Sequence 2, Application US/09046736
Patent No. 6090582
GENERAL INFORMATION:
APPLICANT: KIRKLY, KRISTINE
APPLICANT: ERICKSON-MILLER, CONNIE
TITLE OF INVENTION: Sialoadhesin Family Member-3
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,736
FILING DATE: 24-MAR-1998
CLASSIFICATION: 514
CLASSIFICATION: 514
APPLICATION DATA:
APPLICATION NUMBER: 60/041,885
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Presbia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GR-50019
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAK: 610-407-0701
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-046-736-2

Query Match 5.6%; Score 85; DB 3; Length 467;
 Best Local Similarity 19.8%; Pred. No. 1.8; Matches 59; Conservative 39; Mismatches 116; Indels 84; Gaps 11;

QY 6 TGCAGGAGLMTVGMWLLAG--LQSARGTNVTVAVDQGLAHGGEGREETERNDSETAENY 62
 Db 160 SGCFQNLTCSCVPWACEQGTPPMISWNGTISVSP----- 191

QY 63 APPETDVSNNVNKVKEFGRMCTVTC----GIGV--REVLTNGCPGGSCKCVRVE 114
 Db 192 PHPSTTRSVLTLIPOPHGNTSLTCQVTLPGAGVTRNTIQNVSYP--PQLTVTFQ 249

QY 115 CRGPTDCGWMGPISSEI--ESVLAC-IHTSPLNPKMKLRLQDQSIILVNDSAIL 170
 Db 250 GEGTASTALGNSSLSVLEGGSLSRLVCDAVDNPAPLSWTR-----SLLT 295

QY 171 EVRKSHPLAFECOTDNNEVATIKETVYTSSELQRSS-----PATDA 217
 Db 296 YPSQSNPLVHLQHGD--GFTCRAONLSQHSVNLSQLQEVYGRKMRPVSGV 351

QY 218 ALIVLVTIGVITCVRIFPLIPIINWAAVKWFAGAKSTPEVOSBOSVYKDSFL 275
 Db 352 LIGAVGGAGATLAVLFLSCVCPVIPV-----SCRKKSRPAADVGDVEMKDANT 401

RESULT 5 US-09-949-016-7821 Application US/09949016

; Sequence 7821, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 7821
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7821

Query Match 5.6%; Score 85; DB 4; Length 596;
 Best Local Similarity 25.7%; Pred. No. 2.6; Matches 43; Conservative 23; Mismatches 55; Indels 46; Gaps 9;

QY 46 EGEETEENND-SETARNYAPPETDVSNNVNKVKEFGRMCTVTCGIGV--REVLTNGCPGG 104
 Db 229 EGATGVSASD-TVBCVLPSKQPEENDQGV-----AGKDRSKEL---G 274

QY 105 ESKCVVURVEBECRGTPCGWMGPISSELESVRLACIHTSPLNPKM-----W-----151
 Db 275 KAAQDITKDER---PGDGRPRKEPCGYDPNALYICRQPHRN-RFMICCDRCBEWFHGD 330

QY 152 -----KLRLQDQSIILVNDASATLEVRKSHPLAFECOTDNNE 190
 Db 331 VGISEARGRLLERENGEDYICPN-CTLIQVQDETH----SETADQO 371

RESULT 7 US-08-311-731A-158 Application US/08311731A

; Sequence 158 Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; TITLE OF INVENTION: NUCICIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAB FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411

RESULT 6 PCT-US9-13975-72 Application PC/TUSS9513975
; Sequence 72, Application PC/TUSS9513975
; GENERAL INFORMATION:
; APPLICANT: Cochran, Mark D.
; APPLICANT: McDonell, Michael W.

CORRESPONDENCE ADDRESS:
 ADDRESSEER: WOLF, GREENFIELD & SACKS, P.C.
 STREET: 600 ATLANTIC AVENUE
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02210

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/311,731A
 FILING DATE:
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: GATES, EDWARD R.
 REGISTRATION NUMBER: 31,616
 REFERENCE/DOCKET NUMBER: C0044/7125
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617/720-3500
 TELEFAX: 617/720-2441

INFORMATION FOR SEQ ID NO: 158:
 SOURCE/CHARACTERISTICS:
 LENGTH: 618 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: YES
 ORIGIN: ORGANISM: Mycobacterium leprae
 US-08-311-731A-158

Query Match 5.5%; Score 83.5; DB 4; Length 618;
 Best Local Similarity 24.1%; Pred. No. 4; Mismatches 60; Conservative 30; Indels 57; Gaps 14;

QY 4 RGTGCGAGLMLTVGWL--LLAGLQSARG--TNTAVDAGLAHGERGER-ETENNSET 58
 Db 58 RALANQAGVKTGSMRKSBLIAIESCRGQANGTSVNDGSPSRDHGSATAISTEALAOE 117

QY 59 AENYAPPETEDVSNRNVKEYEFFGMCTVTCGIGGVREVL----TNGCPGGESKC 108
 Db 118 BQNYVAEVSVRERRGASREAD----VTAGHTSAATESDCQGTADDITLQSQSD- 171

QY 109 VVRVBECRGPTDCGGWGPKISSESLSBSVRLACIHTSPL-----NPKYMWKLRL 155
 Db 172 -TKTER-RGP-DVNDGGEVQOSSLQ-----PRGDDGGERQGRGRGRFRDRRR 221

QY 156 QDQQSILVNLNSALLRKES--HPLAFECPTDNNNEIVATIKP----TYTSSBLQMR 208
 Db 222 GERS----GDQAELRQDDVYQPVAGILDVIDVNAYFVRTSGYLAGPHDVYVMSM-VR 275

QY 209 RSSLPATDA 217
 Db 276 KNGLRKGDA 284

RESULT 9

US-09-248-796A-14534

; Sequence 14534, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13
 NUMBER OF SEQ ID NOS: 28208
 SEQ ID NO 14534
 LENGTH: 519
 TYPE: PRT
 ORGANISM: Candida albicans
 US-09-248-796A-14534

Query Match 5.4%; Score 83; DB 4; Length 519;
 Best Local Similarity 22.9%; Pred. No. 3.5.; Mismatches 30; Conservative 30; Indels 24; Gaps 5;

QY 127 ISESLRSVRACIHTSPLANKPKYMKULLAQDQOSITLVNDSAILEVRKSHPLAECDT 186
 Db 25 LRETTETAIISLVSIFNRSH----KQEESTLSTNN-----NNNN 66

QY 187 DNNEIVATKPTVVTYVSSELQMRASSLPAATDRLFV-LTIGVIIIC--VFIIFLIFIIN 243
 Db 67 DNNEENENENAVHPHSISOSRKADMNRKLUKPOWIGAIGLIGLICPIGICIFULIFYFG 126

Qy 244 --WAIAKAW 251
 Db 127 QDYWSYSTERW 137

RESULT 9

US-09-134-001C-4799

; Sequence 4799, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 4799

; LENGTH: 366

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-4799

Query Match 5.4%; Score 82.5; DB 3; Length 366;
 Best Local Similarity 19.0%; Pred. No. 2.3.; Mismatches 47; Conservative 41; Indels 79; Gaps 11;

QY 21 LAGLQSARGNTAAVODAGLAHGERGERETENNDS-----ETAENTAPPETDVSN 72
 Db 107 IPDISGYDTRTRITKRNLYTRAG---FDNKONIQEVEQLKTA-IPRDEVOTVR 161

QY 73 R-----NVKEVERFGMCTV-----CGIGREVILNG 100
 Db 162 KIPVSYSGISLSVWLDFGKQNTVRELVEPLNLRGCVTVWPYDTSAEILGHSPDGVLNS 221

QY 101 CGGESKCVVRVBECRGPTDCGGWK-----PSESLSBSVRLACIHTSPLNR 147
 Db 222 -PGDPDEVDVALDMRGL--GKIPPFICLGHOLPALSQGATSPKMKFGHRA--- 272

QY 148 KOMKKLURDQDOSITLVNDLALEYRKESHLAFEGCTDNNNEIVATIKPVTYTSBLQ 207
 Db 273 NPVKDQIURGK-----IDITSQNHCYSIDESCLSKNTDLE-T-HAINDGTVEGL 320

Qy 208 RSSLPKA 214
 Db 321 RHKELPKA 327

RESULT 10

US-09-513-783A-142
 Sequence 142, Application US/09513783A
 Patent No. 6416959

GENERAL INFORMATION:

APPLICANT: Giuliano, Kenneth A.

ATTORNEY/R: Ravi

TITLE OF INVENTION: A System for Cell Based Screening

FILE REFERENCE: 97-022-L1

CURRENT APPLICATION NUMBER: US/09/513,783A

CURRENT FILING DATE: 2000-02-25

NUMBER OF SEQ ID NOS: 180

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 142

LENGTH: 566

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Size exclusion

OTHER INFORMATION: target sequence

US-09-513-783A-142

Query Match 5.2%; Score 80; DB 4; Length 566;

Best Local Similarity 22.1%; Pred. No. 8.7;

Matches 53; Conservative 32; Mismatches 101; Indels 54; Gaps 7;

Query 2 SPRGTGCSAGLIMTVGMLLAGIQLQSARGNTVTAVODAGLAHEGEGEBETENDSETAEN 61

Db 344 SPKETIETLPIKMD----LAPPEDVLLTKETELAPAKGMVSLSEBALAKNDVSAEI 398

Query 62 YAPPETEDVSIRNWKVEVRFGMCT-----VTCGGIGREVILNGCAGGES 106

Db 399 PVAQET-----WVSETEVVLATEVLPSPDPTITLKDVTPLAEARPLVDMTPSLET 451

Query 107 KCVVRBECRGITDCGNGK-----PISESLESVRACIHTISPLNRPKWMKLLRQDQO 159

Db 452 ENTLG-KETAPPTENGMAKOMSPLESEBVTLGKVDTPLKSEVNLKAFENNTPLSREBT 510

Query 160 SITLVDSATLAVRKSHPLAFCDTLDNNETIVATIKFTVTTSEQLQRSSLPATDAAL 219

Db 511 SVKDMSPSAETEA----PLAKNAD-----LHSGETLVDNSMAPASDL 551

OTHER INFORMATION: target sequence
 US-09-430-656-142

Query Match 5.2%; Score 80; DB 4; Length 566;

Best Local Similarity 22.1%; Pred. No. 8.7;

Matches 53; Conservative 32; Mismatches 101; Indels 54; Gaps 7;

Query 2 SPRGTGCSAGLIMTVGMLLAGIQLQSARGNTVTAVODAGLAHEGEGEBETENDSETAEN 61

Db 344 SPKETIETLPIKMD----LAPPEDVLLTKETELAPAKGMVSLSEBALAKNDVSAEI 398

Query 62 YAPPETEDVSIRNWKVEVRFGMCT-----VTCGGIGREVILNGCAGGES 106

Db 399 PVAQET-----WVSETEVVLATEVLPSPDPTITLKDVTPLAEARPLVDMTPSLET 451

Query 107 KCVVRBECRGITDCGNGK-----PISESLESVRACIHTISPLNRPKWMKLLRQDQO 159

Db 452 ENTLG-KETAPPTENGMAKOMSPLESEBVTLGKVDTPLKSEVNLKAFENNTPLSREBT 510

Query 160 SITLVDSATLAVRKSHPLAFCDTLDNNETIVATIKFTVTTSEQLQRSSLPATDAAL 219

Db 511 SVKDMSPSAETEA----PLAKNAD-----LHSGETLVDNSMAPASDL 551

RESULT 11

US-09-430-656-142

Sequence 142, Application US/09430656

Patient No. 6756207

GENERAL INFORMATION:

APPLICANT: Barr, Philip J.

APPLICANT: Brake, Anthony J.

APPLICANT: Kaufman, Rhadal J.

APPLICANT: Tekamp-Olson, Patricia

APPLICANT: Wasley, Louise

APPLICANT: Wong, Polly A.

TITLE OF INVENTION: Expression of PAGE in Host Cells and

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSE: Howson & Howson

STREET: Spring House Corporate Center, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

ZIP: U.S.A.

COUNTRY: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-POS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/885,972A

FILING DATE: 19920520

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/621,092

FILING DATE: 26-Nov-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,859

FILING DATE: 29-Nov-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/621,443

FILING DATE: 29-Nov-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/621,457

FILING DATE: 30-Nov-1990

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: G15181A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 142
 LENGTH: 566
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Size exclusion

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 794 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

MOLECULE TYPE: protein

US-07-885-972A-2

Query Match Similarity 5.2%; Score 80; DB 1; Length 794;

Best Local Similarity 21.7%; Pred. No. 15; Mismatches 111; Index 132; Gaps 18; Matches 75; Conservative 27; MisMatches 111; Indexs 132; Gaps 18;

QY 1 MSPRPGCSAGLIMTVGWLILAGL---OSARGNTNTAAVODAGLAHEGEGBETENDSE 57
506 VSPMGTRST-----LIAARPHDYSADGFNDWAFMTHSWEDBPSGEWVBIENTS 555

QY 58 TAENY-----APPE-----TEUDSNRNWVKEVTEFGM---CTVTGCG 89

Db 556 BANNYGTLTKEPLVLYGTAPEGGLPVPPBESGCKTILTSSOACVVCVBEGFSLHQKSCVQHCP 615

QY 90 IGV-----EVILNGCPGGEKCVVRVEBGRGP---TDCGMKPISLES 133

Db 616 PGRAFOVLDTHYSTENDVETRASVYCARPHASCAT---COGRALITDC-LSCRPSHDSLDP 670

QY 134 VLACHTHSPLNPKYMWKLURQDQOSIILVNDSAILEVKESHPLAFECOTLDNNNEVA 193

Db 671 VEQTC-----SRQSOSS-----RESP-----QQQP 692

QY 194 TIKFTWYTSSRLQ--MRRSSLPATDAALIFLVLTIGVIVICVI-IFLLIFIINNAVKA 249

Db 693 RLPPEVAGORLRAGLIPSLPHEPVVAGL-----SCARIVLVLVFVTFVLVQLRSGFS 743

QY 250 FWGAKASTPVSQBOSSVRYKDSISLDQIPTEMPCHDDALLEWNE 294

Db 744 FRGVKVT---MDRGILISKG-----LPPE-----AWQE 769

RESULT 13

US-07-885-972A-4

Sequence 4, Application US/07885972A

PATENT NO. 5460950

GENERAL INFORMATION:

APPLICANT: Barr, Philip J.

APPLICANT: Brake, Anthony J.

APPLICANT: Kaufman, Bradal J.

APPLICANT: Tekamp-Olson, Patricia

APPLICANT: Wasley, Louise

APPLICANT: Wong, Polly A.

TITLE OF INVENTION: Expression of PACE in Host Cells and

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

STREET: Spring House Corporate Center, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19477

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/885,972A

FILING DATE: 1990520

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/621,092

FILING DATE: 26-Nov-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/620,859

FILING DATE: 29-Nov-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/621,443

FILING DATE: 29-NOV-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/621,457

FILING DATE: 30-NOV-1990

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: G15181A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

SEQUENCE CHARACTERISTICS:

LENGTH: 794 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

US-07-885-972A-4

Query Match Similarity 5.2%; Score 80; DB 1; Length 794;

Best Local Similarity 21.7%; Pred. No. 15; Mismatches 111; Index 132; Gaps 18; Matches 75; Conservative 27; MisMatches 111; Indexs 132; Gaps 18;

QY 1 MSPRPGCSAGLIMTVGWLILAGL---OSARGNTNTAAVODAGLAHEGEGBETENDSE 57

Db 506 VSPMGTRST-----LIAARPHDYSADGFNDWAFMTHSWEDBPSGEWVBIENTS 555

QY 58 TAENY-----APPE-----TEUDSNRNWVKEVTEFGM---CTVTGCG 89

Db 616 BANNYGTLTKEPLVLYGTAPEGGLPVPPBESGCKTILTSSOACVVCVBEGFSLHQKSCVQHCP 615

QY 90 IGV-----EVILNGCPGGEKCVVRVEBGRGP---TDCGMKPISLES 133

Db 616 PGRAFOVLDTHYSTENDVETRASVYCARPHASCAT---COGRALITDC-LSCRPSHDSLDP 670

QY 134 VLACHTHSPLNPKYMWKLURQDQOSIILVNDSAILEVKESHPLAFECOTLDNNNEVA 193

Db 671 VEQTC-----SRQSOSS-----RESP-----QQQP 692

QY 194 TIKFTWYTSSRLQ--MRRSSLPATDAALIFLVLTIGVIVICVI-IFLLIFIINNAVKA 249

Db 693 RLPPEVAGORLRAGLIPSLPHEPVVAGL-----SCARIVLVLVFVTFVLVQLRSGFS 743

QY 250 FWGAKASTPVSQBOSSVRYKDSISLDQIPTEMPCHDDALLEWNE 294

Db 744 FRGVKVT---MDRGILISKG-----LPPE-----AWQE 769

RESULT 14

US-08-865-203-2

Sequence 2, Application US/08865203

PATENT NO. 5935815

GENERAL INFORMATION:

APPLICANT: van de Ven, Willem Jan Marie

APPLICANT: van den Ouwendijk, Anna Maria Wilhelmina

APPLICANT: Van Duljhaven, Johannes Lambertus Petrus

APPLICANT: Robroek, Antonius Johannes Maria

APPLICANT: Koning, Piet Nico Maria

TITLE OF INVENTION: Pharmaceutical Composition Having An Endoproteolytic Activity; A Process for Endoproteolytically Processing (Precursor)

TITLE OF INVENTION: Proteins And For The (Micro) Biological Production Of Proteins

TITLE OF INVENTION: Production Of Proteins

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOFFMANN & BARON, LLP

STREET: 350 Jericho Turnpike

CITY: Jericho

STATE: New York

COUNTRY: U.S.A.

ZIP: 11753

Mon Apr 18 12:47:48 2005

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Page 8

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